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                                                             August 11, 2004, 17:57:26; Search time 18 Seconds (without alignments)
184.984 Million cell updates/sec
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Sequence 5, A
Sequence 4, A
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Sequence 15,
Sequence 30,
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-378-535-9
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US-08-01206-1
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US-08-01206-1
US-08-01-13A-6
US-08-01-13A-6
US-09-349-532-15
US-09-349-532-34
US-09-940-133A-4
US-09-940-133A-4
US-09-940-133A-4
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-018-545-3
US-09-114-399-3
US-09-608-636A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-729-598-4
US-08-819-867-9
US-08-819-867-27
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US-08-670-999-3
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                                                                                                                                                                             682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
                                          using sw model
                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                      US-09-540-843-11
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Match Length
                                           nucleic search,
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No.
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28	Sequence 27, Appl Sequence 14, Appl Sequence 16, Appl Sequence 16, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 17, Appl Sequence 21, Appl Sequence 29, Appl Sequence 29, Appl Sequence 11, Appl Sequence 21, Appl	Use in the Treatment	0; Gaps 0;
28 6 100.0 39 6 100.0 31 6 100.0 32 6 100.0 33 6 100.0 34 6 100.0 35 6 100.0 36 100.0 37 6 100.0 38 6 100.0 38 6 100.0 40 6 100.0 41 6 100.0 42 6 100.0 43 6 100.0 44 6 100.0 44 6 100.0 44 6 100.0 45 6 100.0 46 100.0 47 6 100.0 48 6 100.0 49 6 100.0 40 6 100.0 41 6 100.0 42 6 100.0 43 6 100.0 44 6 100.0 45 6 100.0 46 100.0 47 11LLB OF INVENTION: TITLE OF INVENTION INVENTION TRELEPAR: TELEPHONE: 515-288 TYPE: OLDIOGY: TYPE:	08-630-019A-27 09-06444-14 08-1838-545.16 09-349-532-16 08-192-300-18 08-531-743.10 08-630-019A-8 08-638-545-7 08-838-545-17 08-838-545-17 08-838-545-29 08-934-532-11 09-349-532-17 09-349-532-17	ALIGNMENTS  197A  10. Oligodeoxyribonuclectides and Crelomeric Sequences for r and Other Diseases  Thomte, Voorhees, & Sease  10. Version #1.30  #1.0, Version #1.30  mmc 63092  acid  Score 6; DB 1; Length 6;	Pred. No. 8.7e+07; 0; Mismatches 0; Indel
28 6 100.0 39 6 100.0 31 6 100.0 32 6 100.0 33 6 100.0 34 6 100.0 35 6 100.0 36 100.0 37 6 100.0 38 6 100.0 38 6 100.0 40 6 100.0 41 6 100.0 42 6 100.0 43 6 100.0 44 6 100.0 44 6 100.0 44 6 100.0 45 6 100.0 46 100.0 47 6 100.0 48 6 100.0 49 6 100.0 40 6 100.0 41 6 100.0 42 6 100.0 43 6 100.0 44 6 100.0 45 6 100.0 46 100.0 47 11LLB OF INVENTION: TITLE OF INVENTION INVENTION TRELEPAR: TELEPHONE: 515-288 TYPE: OLDIOGY: TYPE:	м м м м н N м м м м м м м м м м м м м м	US/0838 US/0838 N. B. N. B. N. B. Of Canc 21 S.S. McKee, Suite 3 AC Compatib PC-DOS/ PC-DOS/ PC-DOS/ NATA: US/08 ATA: US/08 ATION: S.33/ ATION: S.33/ ATION: S.33/ ATION: S.31/ ATION: S.31	100.0%; ive
SOUL Page 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		3, Applica 3, Applica 3, Applica 3, S643890 I. S643890 I. S643890 OF INVENTI I. Des Moi ESSERS Za ES	Simi 6;
AD we		RESULT 1 US-08-391- 1 Sequence 1 Patent h APPLI TITLE TITLE NUMBH STI STI STI STI ATTOI ANTI US-08-381- US-08-381- ANTI US-08-381- US-08-381- ANTI US-08-381- ANTI US-08-381- US-08-381- ANTI US-08-381- US-08-381- ANTI US-08-381- US-0	Best Lo

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100.0%; Score 6; DB 1; Length 6; 100.0%; Pred. No. 8.7e+07; ive 0; Mismatches 0; Indels
   THERAPY AND DIAGNOSIS OF
CONDITIONS RELATED TO TELEOMERE
LENGTH AND/OR TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READALE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 6.5" DIskette, 1.44 Mb
COMPUTER: 1.5" C
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPPRATING SYSTEM: IBM P.C. DOS 5.0
TITLE OF INVENTION: THERAPY AND D.
TITLE OF INVENTION: CONDITIONS REI
TITLE OF INVENTION: LENGTH AND/OR
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 6; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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STATE: California
                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A. ZIP: 90071
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APPLICANT: Mara, John E.
TITLE OF INVENTION: Synthteic Oligodeoxyribonucleotides
TITLE OF INVENTION: Which Mimic Telometic Sequences for Use in the Treatment
TITLE OF INVENTION: of Cancer and Other Diseases
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Zarely, McKee, Thomte, Voorhees, & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,097A
FILING DATE: 31-JAN 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: NEDE-1, Heidi S
REGISTRATION NUMBER: 37,719
REFERENCE/POCKET NUMBER: 37,719
REGISTRATION NUMBER: 37,719
TELEPHONE: 515-288-367
TELEPHONE: 515-288-367
TELEFRAX: 515-288-367
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                US-08-381-097A-5/c; Sequence 5, Application US/08381097A; Patent No. 5643890
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Michael J. McEachern
Homayoun Vaziri
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Woodring E. Wright
Elizabeth Blackburn
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Calvin B. Harley
Scott L. Weinrich
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Matches 6; Conservative
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STRANDEDNESS: single
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MOLECULE TYPE: Ot
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APPLICANT:
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APPLICANT:
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Query Match

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPREMING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 514
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/151,477A
FILING DATE: NO. 5836644ember 12, 1993
FILING DATE: NO. 5836644ember 12, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: MARCH 24, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WAIDLING Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 32,327
FELECOMMUNICATION INFORMATION:
TELECAMONICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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NAME: Nebel, Heidi S.
REGISCRATION NUMBER: 37,719
REFRENCE/DOCKET NUMBER: unmc
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Iowa COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 6 base pairs
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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APPLICANT: Michael J. McEachern
APPLICANT: Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO TELEOMERE
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 6; DB 1; Le
100.0%; Pred. No. 8.7e+07;
    SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION NUMBER: US/08/337,684
FILING DATE: NO. 5686306ember 10, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/151,477
FILING DATE: NO. 5686306ember 12, 1993
APPLICATION NUMBER: 08/153,051
FILING DATE: NO. 5686306ember 12, 1993
APPLICATION NUMBER: 08/153,051
FILING DATE: NO. 5686306ember 12, 1993
APPLICATION NUMBER: 08/000,952
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                              APPLICATION NUMBER: 08/060,952
FILING DATE: May 13, 1993
APPLICATION NUMBER: 08/038,766
FILING DATE: Maxch 24, 1993
APPLICATION NUMBER: 07/882,438
FILING DATE: May 13, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/085
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-151-477A-4/c; Sequence 4, Application US/08151477A; Patent No. 5830644; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Michael D. West
Jerry W. Shay
Woodring E. Wright
Elizabeth Blackburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nam Woo Kim
Calvin B. Harley
Scott L. Weinrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
US-08-337-684-2
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APPLICANT:
APPLICANT:
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Gaps
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                                                           APPLICANT: Woodring B. Wright
APPLICANT: Blizabeth H. Blackburn
APPLICANT: Nam Woo Kim
APPLICANT: Homeyoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: CONDITIONS RELATED TO
TITLE OF INVENTION: TEOLOMERE LENGTH AND/OR
TITLE OF INVENTION: TELOMERASE ACTIVITY
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
ORPRATING SYSTEM: IBM C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: 08/153,051
FILING DATE: NO. 6007989ember 12, 1993
Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
Nam Woo Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Michael D. West
Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 27, Application US/08819867; Patent No. 6007989; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-819-867-9
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-819-867-27/c
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                         APPLICANT
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                                                               Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: NO. CONTRY! USA

ZUP: 27627

ZUP: 27627

COMPUTER READABLE FORM:

FIGURATING TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOCTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NDATA:
APPLICATION NUMBER: US/08/729,598

FILING DATE: 11-OCT-1996

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Biswas, Sorojini J.
REFERENCE/DOCKET 139,111

FILECOMMUNICATION INFORMATION:
TELEPHONE: (919) 854-1400

TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 854-1401

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENTORMATICS:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hardin, Charles C.
APPLICANT: Brown II, Bernard A.
APPLICANT: Broberts, John J.
APPLICANT: Roberts, John J.
TITLE OF INVENTION: Antibodies That Selectively Bind
TITLE OF INVENTION: Quadruplex Nucleic Acids
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sorojini J. Biswas
STREET: P.O. Box 37428
                                                           Ouery Match 100.0%; Score 6; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08729598
Patent No. 6001657
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Raleigh
STATE: No. 6001657th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08819867
Patent No. 6007989
GENERAL INFORMATION:
APPLICANT: Michael D. West
APPLICANT: Calvin B. Harley
APPLICANT: Scott L. Weinrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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Matches 6; Conserv
                                                                                                                                                 1 TTAGGG 6
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; ANTI-SENSE:
US-08-670-999-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-08-819-867-9
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COMPUTER: IN PC COMPATIBLE
COMPUTER: IN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/630,019A
FILING DATE: 09-JUN-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/018,545
FILING DATE: CONCURRENTLY Herewith
                                                                                                                                                                                                               ATURNEY AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001600US
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara 8.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UISB:654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09018545
Patent No. 6087493
                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
                   ZIP: 94111-3834
COMPUTER READABLE FORM:
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STREET: F.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: D. STATE: Texas COUNTRY: U.S. 77210
                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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APPLICANT: Wright, Woodring B.

APPLICANT: Paryszek, Mieczyslaw A.

APPLICANT: Corey, David

APPLICANT: No. 6015710cn, James C.

TITLE OF INVENTION: Modulation of Mammalian Telomerase by

TITLE OF INVENTION: Peptide Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6;
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ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Two Embarcadero Center, Eighth Floor
                                        THERAPY AND DIAGNOSIS OF
APPLICANT: Nam Woo Kim
APPLICANT: Homayoun Vaziri
APPLICANT: Homayoun Yaziri
THILE OF INVENTION: CONDITIONS RELATED TO
TITLE OF INVENTION: TEOLOMERE LENGTH AND/OR
TITLE OF INVENTION: TEOLOMERE LENGTH AND/OR
NUMBER OF SEQUENCES: 80
                                                                                                                                                                                                                                                                                                                                                 CORRECT IRM COMPATIBLE
COMPUTER: IRM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/819,867
FILING DATE: March 14, 1997
CLASSIFICATION: 435
PRIOR APPLICATION UNMER: 08/153,051
FILING DATE: NO. 6007989ember 12, 1993
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224/232
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                                                                                                                                                                 E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/ACERNT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213, 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   San Francisco
                                                                                                                                                                                                       Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
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90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Shay,
                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-819-867-27
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                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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DESCRIPTION: /desc = "peptide nucleic acid (PNA),
DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
DESCRIPTION: glycine amino nitrogen through a methylenecarbonyl linker"
                                                                                                                                                                                                                                                               o,
                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                 100.0%; Score 6; DB 3; Length 6; 100.0%; Pred. No. 8.7e+07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Wheelhouse, Richard T.
APPLICANT: Hurley, Laurence H.
ITILE OF INVENTION: PORPHYRIN COMPOUNDS AS TELOMERASE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS RELATED TO TECLOMERE LENGTH AND/OR TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FREESEG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
                          PRIOR APPLICATION NUMBER: 2000-06-30

PRIOR PLING DATE: 2090-06-30

PRIOR FILING DATE: 1999-07-10

PRIOR PLILING DATE: 1999-07-10

PRIOR APPLICATION NUMBER: JP 11-187616

PRIOR APPLICATION NUMBER: JP 11-307576

PRIOR PLING DATE: 1999-10-28

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PATENTIN VETSION 3.1

SEQ ID NO 1

LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
                   CURRENT APPLICATION NUMBER: US/09/608,636A CURRENT FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 Weat Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/819,867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-Aug-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: oligonucleotide US-09-608-636A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09378535; Patent No. 6551774; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calvin B. Harley
Scott L. Weinrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Michael D. West
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                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nam Woo Kim
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                      FEATURE:
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IITLE OF INVENTION: Telomerase Inhibitors and Methods of Their Use
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                                                                                                                                                                                                                                   Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Porter, Thomas R.
APPLICANT: Iversen, Patrick L.
APPLICANT: Iversen, Patrick L.
APPLICANT: Mayer, Gary D.
TITLE OF INVENTION: Targeted Site Specific Drug Delivery
TITLE OF INVENTION: Compositions and Method of Use
TITLE OF INVENTION: Compositions and Method of Use
CURRENT APPLICATION NUMBER: US/09/114,399
PRICE APPLICATION NUMBER: US 08/015,495
PRICE APPLICATION ON UNUMBER: US 08/615,495
PRICE APPLICATION ON UNUMBER: US 08/615,495
                                                                                                                                                                                                                                100.0%; Score 6; DB 3; L6 100.0%; Pred. No. 8.7e+07;
                                                                                                                                                                                                                                                                          0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kyowa Hakko Kogyo Co., Ltd.
Chin, Allison C.
Holcomb, Ryan C.
Platyszek, Mieczyslaw A.
Singh, Upinder
Tollam, Richard L.
Akama, Tsutcmu
Kanda, Yutaka
Asai, Akira
Yamashita, Yoshinori
Endo, Kaori
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Patent No. 6518268
GENERAL INFORMATION:
APPLICANT: Geron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09114399 Patent No. 6245747
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                   TELEPHONE: (512) 418-30C
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geron Corporation
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                                                                                                   LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                   ; TOPOLOGY: linear
US-09-018-545-3
                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
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US-09-608-636A-1
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LENGTH: 6
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APPLICANT
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100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homayoun Vaziri
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONDITIONS RELATED TO
TEOLOMERE LENGTH AND/OR
TELOMERASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTENG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/378,535
FILING DATE: 20-Aug-1999
CLASSIFFCATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
TILING DATE: <UNKNOWN>
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,561
REFERENCE/DOCKET NUMBER: 224/232
                                                                                                                                                                                              TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calvin B. Harley
Scott L. Weinrich
Catherine M. Strahl
Michael J. Mceachern
Jerry Shay
Woodring E. Wright
Elizabeth H. Blackburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 488-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE_CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 27, Application US/09378535; Patent No. 6551774
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Michael D. West
                                                                                                                              LENGTH: 6 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             storage
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                                                                                                                                                                                                                                                                                                                                                                   1 TTAGGG 6
                                                                                                                                                                                                                                                                                                                                                                                                           1 TTAGGG 6
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LENGTH: 6 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

Cuery Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
Best Local Similarity 100.0%; Pred. No. 8.7e+07;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 1 TTAGGG 1

Db 6 TTAGGG 1

Search completed: August 11, 2004, 19:33:24

Search completed: August 11, 2004, 19:33:24
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(0,10/sN) XUD/8 @60d S!U]

August 11, 2004, 17:38:14; Search time 380.903 Seconds (without alignments) 682.741 Million cell updates/sec OM nucleic - nucleic search, using sw model US-09-540-843-11 1 ttaggg 6 Title: Perfect score Sequence: Run on:

Total number of hits satisfying chosen parameters: 3470272 seqs, 21671516995 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

2199298

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200

GenEmbl:\* Database

em\_pl:\*
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em\_htg\_other:\*
em\_htg\_other:\*
em\_htg\_pln:\*
em\_htg\_pln:\* gb ba: \*
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gb om: \*
gb pat: \*
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g em\_ov:\* em\_pat:\* em\_ph:\* em\_mu:\* em or:\*

Pred. No. is the number of results predicted by chance to have a

em\_htgo\_other:\* em\_htg\_vrt:\*
em\_sy:\*
em\_htgo\_hum:\*
em\_htgo\_mus:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AXO55801 Sections	58275 Segment	75285 Segment	8763 Sequenc	3764 Segment	98	9 Modulati	63 Modulati	7 Modulati			638	0 1	BD24031 Freparati	Hu	Sequ	9989	AR390657 Sequence		AA1321// Sequence AX153381 Semishoo	AX153382 Segrence	83				BD023724 Method fo	1041	2		4	BD071062 Modulatio	o numan	5034 Semience	5486	5487	9195	206 S	1904 Sequenc	19 Se	14804 S	AR301476 Sequence
SUMMARIES	ū	AX055801	AX05827	AX175	AX26876	AX2687	BD23008		BD07106	BD07106	BD0710	AR0264	BD2386	BD2389	BD240276	E36980	AR24350	AR33686									BD023724				BD071			AR016034		AR02648	AR0591	AR07550	AR161	131749	ARZI	AK3014/
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Sequence 5 from Patent W00073420. AX055801. AX055801.1 GI:12228914 RESULT 1
AX055801/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

PAT 13-JAN-2001

linear

DNA

ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL

synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 6)
Hahn, W.C. and Weinberg, R.A.
Creation of human tumorigenic cells and uses therefor
Patent: WO 0073420-A 5 07-DEC-2000;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; DANA-FARBER

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PAT 29-OCT-2001
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Best Local Similarity 100.0%; Pred. No. 7.2e+09;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                             Indels
Length 6;
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100.0%; Pred. No. 7.2e+09;
iive 0; Mismatches 0;
 100.0%; Score 6; DB 6; Li
100.0%; Pred. No. 7.2e+09;
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/mol_type="genomic DNA"
| Do xref="taxon:32630"
/note="Synthetic DNA Fragment"
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/organism="synthetic construct"
/mol type="qenomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                               DNA
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Patent: WO 0174342-A 12 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)
                                                                                                                                                                                                                                                                                             Gilchrest,B.A., Yaar,M. and Eller,M. Use of locally applied dna fragments Patent: WO 0174342-A 11 11-OCT-2001; TRUSTEES OF BOSTON UNIVERSITY (US) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gilchrest, B.A., Yaar, M. and Eller, M.
                              0; Mismatches
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Sequence 12 from Patent WO0174342.
AX268764
                                                                                                                                                             6 bp
Sequence 11 from Patent W00174342.
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                                                                                                                                                                                               AX268763.1 GI:16541835
                                                                                                                                                                                                                                       synthetic construct
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artificial sequences.
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synthetic construct
artificial sequences.

1 (bases 1 to 6)
Au,J.L. and Wientjes,G.
Compositions active in telomere damage comprising a taxane and
telomerase inhibitor
Patent: WO 0074667-A 10 14-DEC-2000;
Au, Jessie L.S. (US); Wientjes, Guillaume (US)
Location/Qualifiers
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artificial sequences.
1 (bases)
Phillips,N.C. and Filion,M.C.
Therapeutically useful synthetic oligonucleotides
Batent: WO 0144465-A 49 21-JUN-2001;
Bioniche Life Sciences Inc. (CA)
Location/Qualifiers
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100.0%; Pred. No. 7.2e+09;
cive 0; Mismatches 0;
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Sequence 10 from Patent WO0074667.
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            CANCER INSTITUTE, INC.
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Modulation of mammalian telomerase by peptide nucleic acids.

Modulation of mammalian telomerase by peptide nucleic acids.

Datent: JP 2001517929-A 29 09-OCT-2001;

GBRON CORP

OB Unidentified

NN JP 2001517929-A/29

PD 9-OCT-2001

PP 09-APR-1997 UP 1997536487

PR 09-APR-1996 US 08/630019

PI JRRNY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID PI UAMES C NORTON

PC CONTAL 4/00, AGIX38/16, C12Q1/68

CC Strandedness: Single;

CC TOPOLOGY: Linear;

CC TOPOLOGY: Linear;

CC TOPOLOGY: Linear;

CC TOPOLOGY: Linear;

CC TOPOLOGY: Linear;
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linkages are replaced by N-(2-aminoethyl)glycine units linked
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                                                                                                                                  /organism='Unidentified'.
Location/Qualifiers
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5.4e+09;
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JP 2001517929-A/29.
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Shay, J.W., Wright, W.E., Piatyszek, M.A., Corey, D. and Norton, J.C.
Modulation of mammalian telomerase by peptide nucleic acids
Datent: JP 2001517929-A 15 09-OCT-2001;
OS Unidentified
PN JP 2001517929-A/15
PN JP 2001517929-A/15
PD 09-OCT-2001
PP 09-APR-1996 US 08/630019
PR 09-APR-1996 US 08/630019
PI JAMES C NORTON
PI JAMES C NORTON
PI JAMES C NORTON
C COTMISSOR OS SINGLE;
C C Strandedness: Single;
C Topology: Linear;
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C /desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC)
                                                          BD230086 8 bp DNA linear PAT 17-JUL-2003 BD230086
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I (bases 1 to 8)

Williams, S.R., Kirchner,J.J. and Dubridge,R.B.

Wethod for making complementary oligonucleotide tag sets

Datent: JP 2002528137-A 3 03-SEP-2002;

LINX THERAPETUTCS INC

OS Artificial Sequence

PN JP 2002528137-A/3

PD 03-SEP-2002

PF 01-NOV-1999 JP 200579783

PR 02-NOV-1999 US 60/106662

PI STEVEN R WILLIAMS, JAMES J KIRCHNER, ROBERT B DUBRIDGE PC

C12N15/09,CI2N15/09,CI2N15/09,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2N15/00,CI2
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Modulation of mammalian telomerase by peptide nucleic acids
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/organism="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                              BD230086.1 GI:33039856
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JP 2001517929-A/15.
                                                                                                                                                                                                           Synthetic construct synthetic construct
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Best Local Similarity 100...
6; Conservative
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FH Key
FT source
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RESULT 6
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VERSION
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Gaps

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE

COMMENT

REFERENCE AUTHORS

LOCUS

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Unclassified.

1 (bases 1 to 10)

Windle, B.E., Qiu, M., Chen, S.-F., Fletcher, T.M. and Maine, I.

Windle, B.E., Qiu, M., Chen, S.-F., Fletcher, T.M. and Maine, I.

Rapid and sensitive assays for detecting and distinguishing between processive and non-processive telomerase activities

processive and non-processive telomerase activities

Patent: US 5856096-A 10 05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT 17-JUL-2003
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                                                                                                                                                                                                                                                                                                                               linkages are replaced by N-(2-aminoethyl)glycine units linked
                                                                                                                                                                                                                                                   Topology: Linear, /desc = 'peptide nucleic acid (PNA), where (deoxy(ribose- CC /desc = 'peptide nucleic acid (PNA),
                                       09-OCT-2001
09-ARR-1997 JP 1997536487
09-ARR-1996 US 08/630019
JERRY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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CC to collection to the methylenecarbonyl linker,
FH Key 1. Cocation/Qualifiers
I source ()crganism='Unidentified'.
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100.0%; Pred. No. 5.6e+06;
tive 0; Mismatches 0;
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Seguence 10 from patent US 5856096.
AR026485
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/organism="unknown"
/mol_type="unassigned DNA"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                 C07K14/00, A61K38/16, C12Q1/68
Strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
           JP 2001517929-A/16
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AR026485
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                                                                                                                                                                                                    unclassified.

I (bases 1 to 8)

S shay, J.W., Wright, W.E., Piatyszek, M.A., Corey, D. and Norton, J.C.
Modulation of mammalian telomerase by peptide nucleic acids
D atent: JP 2001517929-A 33 09-OCT-2001;
GERON CORP
OS Unidentified
N JP 2001517929-A/33
PD 09-OCT-2001
PP 09-APR-1997 JP 1997536487
PR 09-APR-1997 LINEARY W SHAY, WOODRING E WRIGHT, MIECZYSLAW A PIATYSZEK, DAVID PI JANES C NORTON
CONTRIVON, AGINSALIE, CI2Q1/68
CC Strandedness: Single;
CC Topology: Linear;
CC Topology: CC Topology: Linear;
CC Topology: CC
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bby DNA linear PAT 27-AUG-2002 Modulation of mammalian telomerase by peptide nucleic acids. BD071067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= 'N = 1-50 peptide nucleic acid nucleobases, selected from U, T, A,
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CC linkages are replaced by N-(2-aminoethyl)glycine un

CC nucleotide bases via glycine amino N through a CC

methylenecarbonyl linker'

CC /mod_base= OTHER

CC /mod_base= OTHER

CC /mod base= OTHER

CC /mod base= OTHER

CC /mod base= OTHER

CC G, i or C'

CC /mod base= OTHER

CC G, i or C'

From U, T, A,

CC G, i or C'

From U, T, A,

CC G, i or C'

From U, T, A,

From Modified base 1

FT modified base 1

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/mol_type="genomic DNA"
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JP 2001517929-A/16.
unidentified
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JP 2001517929-A/33.
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1 (bases 1 to 9)
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Matches

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1 (basea: 1 to 10)

Roberts, B.L. and Shankara, S.
Preparation and use of superior vaccines
Perparation and use of superior vaccines
GENZYME CORP

OS Homo sapiens (human)
PD JP 2002534056-A/358
PD 15-CCT-2002
PP 18-JUN-1999 JP 2000554749
                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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60/089844
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Location/Qualifiers
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JP 2002534056-A/56
15-OCT-2002
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Roberts, B.L. and Shankara, S.
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Homo sapiens (human)
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Roberts, B.L. and Shankara, S. Preparation and use of superior vaccines Patent: JP 2002534056-A 613 15-OCT-2002;
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60/089853
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Location/Qualifiers
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1 (bases 1 to 10)

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Properts 1. and Shankara, S.

Preparation and use of superior vaccines
Patent: JP 2002534056-A 1694 15-OCT-2002;

GENZYME CORP
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/organism='Homo sapiens (human)'.
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/db_xref="taxon:9606"
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1 ttaggg 6 score: Sequence:

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3373863 seqs, 2124099041 residues Searched:

3774412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2001as:\* N\_Geneseq\_29Jan04:\* geneseqn2001bs:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2004s:\* geneseqn1980s:\*geneseqn1990s:\* geneseqn2003as:\* geneseqn2000s:\* geneseqn2002s:\* 9: 10: ٠. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

0	Description						Telomer	Acd25831 Telomere	ıo				æ		6 PNA	PNA	Aat05735 Telomeras			-	Aaa37559 PNA semie		_	
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## ALIGNMENTS

AAT05734 standard; DNA; 6 BP. (first entry) 01-FEB-1996 AAT05734; RESULT 1 AAT05734 

Telomerase oligonucleotide substrate #1.

Telomerase; proliferation; telomere; hybrid; immortalised cell; anaemia; transplantation; cell therapy; treatment; AIDS; leukaemia; lymphoma; ss.

Synthetic.

WO9513383-A1.

18-MAY-1995.

94WO-US013130. 10-NOV-1994; 93US-00151477. 12-NOV-1993; 12-NOV-1993;

(GERO-) GERON CORP. (TEXA ) UNIV TEXAS

UNIV TEXAS SYSTEM.

Wright WE;

West MD,

Shay J,

WPI; 1995-224051/29.

Increasing telomere length in cells - to increase proliferative capacity and therefore delay cellular senescence, useful in cell therapy and transplantation.

Claim 12; Page 29; 38pp; English.

Oligonucleotides AAT05734-7 are examples of telomerase substrates used to increase the proliferative capacity of normal cells that express telomerase activity. The oligonucleotides allow an increase in length of telomeres in normal cells and in hybrids of normal and immortalised cells. The increase in telomere length extends the capacity of cells to replicate, esp. those treated ex vivo and used for transplantation techniques e.g. cell therapy, for the treatment of AIDS, anaemia, leukaemia or lymphoma

(first entry)

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Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; appthosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                                                                                                                                                                                                Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of
                                                                                                                                                                                                                                                                                                                                                                                                                              invention describes inhibition of mammalian epithelial cell
                                   Melanogenesis associated oligonucleotide #12.
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 37; 74pp; English.
                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US010162.
                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-00540843
                                                                                                                                                                                                                                                                                                     Gilchrest BA, Yaar M,
                                                                                                                                                                                                                                                                              (UYBO-) UNIV BOSTON
                                                                                                                                                                                                                                                                                                                            WPI; 2001-626338/72
                                                                                                                                                                                                                                                                                                                                                                                ultra-violet light
                                                                                                                                                                            WO200174342-A2
                                                                                                                                                                                                     11-OCT-2001.
             14-FEB-2002
                                                                                                                                                   Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a mouse telomerase reverse transcriptase (mTERT) enzyme. Compositions containing mTERT can be used in telomere length assays. Isolated mTERT is useful as an immunogen for the production of monoclonal or polyclonal antibodies. The method is useful for assessing the degree of purification and identification of new mTERT species, such as an mTERT allele, homolog or isoform, or to screen for modulators (antagonists and agonists) of telomerase-mediated DNA replication. Antagonists and agonists of mTERT can be used to modify the activity of other telomerase enzymes such as human TERT (hTERT)
                                                                                                                                                                                                                                                                  Telomerase reverse transcriptase; TERT; mouse; telomere length assay; immunogen; enzyme; telomerase-mediated DNA replication; human; ss.
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse telomerase reverse transcriptase (mTERT) enzyme proteins and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 6; DB 2; Length 6; 100.0%; Pred. No. 7e+08; O; Indels
                                                    0; Indels
                           DB 2; Length 6; 7e+08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
   Seguence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;
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                                    100.0%; Preα. ...
ive 0; Mismatches
                            100.0%; Score 6; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 62; 135pp; English
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                                                                                                                                                                                                                                                                                                                                                                                     98WO-US025211
                                                                                                                                                                     AAX80998 standard; DNA; 6 BP.
                                                                                                                                                                                                                                                                                                                                                                                                             97US-00979742
98US-00042460
                                                                                                                                                                                                                      13-SEP-1999 (first entry)
                                                                                                                                                                                                                                                Telomeric repeat sequence.
                                                       6; Conservative
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                              Query Match
Best Local Similarity
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                                                                              1 TTAGGG
                                                                                                         TTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GERO-) GERON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids.
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                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                        Matches
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Eller M;

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The invention describes initiation or mammination between the production of proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce comparation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tunmour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 company, resulting in transient arrest of cell growth, allowing more time corrupts to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other corrupts for the proposition of a processed processed of allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in caused by radiation or chemicals; increase melanin production conformation in epithelial cells (a.g. for treating vitiligo), and to promote apoptosis, in response to DNA damage, in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cells that contain of the reverse complementary sequence of AAS149015, a truncated version of the sequence complementary sequence over-hang sequence (AAS14901), described in the
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100.0%; Pred. No. 7e+08;
iive 0; Mismatches
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Best Local Similarity
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RESULT 4

AAS14916 standard; DNA; 6 BP.

AAS14916/c

RESULT 3

Dp. ð

AAS14916

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Gaps

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Local Similarity 100. nes 6; Conservative

Best Loc Matches

9

Bovine; Bos taurus; EST; expressed sequence tag; totipotence;

development; gene; ss.

WO200194550-A2.

Bos taurus.

13-DEC-2001.

Bovine embryonic germ (EG) cell cDNA EST 990913a CONTIG 1.

(first entry)

03-JUL-2002

ABN73654;

ABN73654 standard; cDNA; 6 BP

ABN73654

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Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer, treat allergically mediated inflammation (aropic or contact dermatitis, allergic thinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligomucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligomucleotide #11, a truncated version of the sequence representing the telomere over-hang sequence (AAS14909) and one of the oligomucleotides used to inhibit mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AAS14909) and one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention describes inhibition of mammalian epithelial cell
                                                                                                                                                                                                                                                                                                           conjunctivitis; allergic rhinitis; vitiligo; ss
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                                                                                                                                       Melanogenesis assocaited oligonucleotide #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US010162.
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  AAS14915 standard; DNA; 6
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                                                                                             14-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                              AAS14915
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The present invention describes an expressed sequence tag (EST), where the EST is an isolated, enriched, or purified nucleic acid sequence representing all or part of a gene, the expression of which, or its complementary sequence, the arguestes the cell as a developmentally competent or incompetent cell. Molecules which induce developmental competence in a cell line are useful for inducing totipotence in one or more cells. Molecules which induce developmental incompetence in a cell line are useful for preventing a full term pregnancy in an animal and inhibiting totipotence. The molecules are also useful for treating a disease in an animal by inducing development of one or more cells of the animal into a specific cell type. The present the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Telomere; ds; cytostatic; human; antipsoriatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                             An expressed sequence tag (EST), the expression of which, o complementary sequence, in a cell identifies the cell as a developmentally competent or incompetent cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 6; DB 6; Length 6; 100.0%; Pred. No. 7e+08; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                      Eilertsen KJ, Pfister-Genskow M,
                                                                                                                                                                                                                                       07-JUN-2001; 2001WO-US018576.
                                                                                                                                                                                                                                                                 07-JUN-2000; 2000US-0209874P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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Matches
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100.0%; Score 6; DB 4; Length 6; 100.0%; Pred. No. 7e+08;
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                      Conservative
         Local Similarity
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                  Matches
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TTAGGG

1 TTAGGG 6

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ACD25831/c RESULT 7

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The invention relates to inhibiting growth of cancer cells, which is independent of presence or activity of telomerase in cells, not requiring the presence or activity of p53 normal function in cells, not regulting in S-phase arrest in cells, and inducing apoptosis in cancer cells, or resulting involving administering a composition comprising oligonucleotides which share at least 50% sequence identity with human telomere overhang repeat, corrigious portion) and is used in a method inhibiting proliferation of epithelial cells in a mammal or preventing/reducing DNA damage in cells of a mammal, where the DNA damage is caused by radiation or DNA-damaging chemicals. The method is useful for inhibiting growth of cancer cells chemicals. The method is useful for inhibiting growth of cancer cells capamous cell carcinoma), for inducing apoptosis in cancer cells in human, promoting differentiation of malignant cells in a mammal, chancing the expression of one or more surface antigens (e.g. MART-1, tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer cells cancer cells in the skin of a mammal, skin cancer in a human with xeroderma or promoting the expression of one or spongiosis, blistering or dyskeratosis in the skin of a mammal, skin cancer in a human with xeroderma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting growth of cancer cells and inducing apoptosis in cancer cells, by administering composition having oligonucleotides that share sequence identity with human telomere overhang repeat.
apoptosis; cancer; p53; epithelial cell proliferation; DNA damage; lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer; squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1; gp-110; hyperproliferative disorder; spongiosis; blistering; dyskeratosis; skin cancer; veroderma pigmentosum; seborrheic keratosis; actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis; arcopic dermatitis; breast cancer; lung cancer; liver cancer; prostate cancer; pancreatic cancer; lung cancer; liver cancer; uterine cancer; colon cancer; brain cancer; bladder cancer; stomach cancer; thyroid cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              basal cell carcinoma) and for treating or preventing pre-cancerous conditions affecting epithelial cells (such as psoriasis and atopic dermatitis) and also the types of cancers of breast, lung, liver, prostate, pancreatic, ovarian, bladder, uterine, colon, brain, cosophagus, stomach, and thyroid. The present sequence is the telomere repeat unit sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 44; Page 9; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-1996; 96WO-US008386.
26-MAR-1998; 98US-00048927.
31-MAR-2000; 200UUS-00540843.
30-MAR-2001; 2001WO-US010162.
                                                                                                                                                                                                                                                                                                                                                                                                       12-APR-2002; 2002US-00122630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GILCHREST B A. ELLER M S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (YAAR/) YAAR M.
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                                                                                                                                                                                                                                                                     Homo sapiens.
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Sequence 6 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 0 Other;

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        100.0%; Score 6; DB 8; Length 6; 100.0%; Pred. No. 7e+08; ive 0; Mismatches 0; Indels
           100.0%; FL.
                             Conservative
Query Match
Best Local Similarity
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Telomere, ds; cytostatic; human, antipsoriatic; dermatological, apoptosis; cancer; p53; epithelial cell proliferation; DNA damage; lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer; squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1; gp-1100; hyperproliferative disorder; spongiosis; blistering; dyskreatosis; skin cancer; xeroderma pigmentoaum; seborrheic keratosis; actinic keratosis; Bowen's disease, basal cell carcinoma; psoriasis; atopic dermatitis; breast cancer; lung cancer; liver cancer;
                                                                                                                                                                         prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer; uterine cancer; colon cancer; brain cancer; oesophageal cancer; stomach cancer; thyroid cancer.
                                                                Telomere repeat unit (complement).
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31-MAR-2000; 2000US-00540843.
ACD25831 standard; DNA; 6 BP.
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                                             (first entry)
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                                                                                                                                                                                                                          Homo sapiens.
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26-MAR-1998;
                                          08-SEP-2003
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                      ACD25831;
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Inhibiting growth of cancer cells and inducing apoptosis in cancer cells, by administering composition having oligonucleotides that share sequence identity with human telomere overhang repeat.

Claim 44; Page 18; 65pp; English.

The invention relates to inhibiting growth of cancer cells, which is independent of presence or activity of telomerase in cells, not requiring the presence or activity of p53 normal function in cells, not resulting in S-phase arrest in cells, and inducing apoptosis in cancer cells, or resulting in cancer cells, involving administering a composition comprising oligonucleotides which share at least 50% sequence identity with human telomere overhang repeat, (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their contiguous portion) and is used in a method inhibiting proliferation of epithelial cells in a mammal or preventing/reducing proliferation of cells in the method is used in a method inhibiting proliferation of chemicals. The method is used in a method inhibiting proliferation of chemicals. The method is used in a method inhibiting growth of cancer cells of squamous cell carcinoma), for inhibiting growth of cancer cells in a mammal, promoting differentiation of malignant cells in a mammal, chuman, promoting differentiation of malignant cells in a mammal, consinase, TRPP-1 or gp-1100) indicative of differentiation of cancer cells (especially melanoma cells) in a human and for treatment of other hyperproliferative disorders (e.g. spongiosis, blisterntiation of a mammal, skin cancer in a human with xerodermal or phagmentosum, seborrheic keratosis, actinic keratosis, Bowen's disease, or basal cell carcinoma) and for treating or preventing pre-cancerous

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conditions affecting epithelial cells (such as psoriasis and atopic dermatitis) and also the types of cancers of breast, lung, liver, prostate, pancreatic, ovarian, bladder, uterine, colon, brain, oesophagus, stomach, and thyroid. The present sequence is the complement of telomere repeat unit sequence found to be less active in melanogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tandem repeats (1-1000) of the telomere are used in a vector for expressing specific genes in plants. They provide 'artificial chromosomes' which are maintained in the nucleus, so are not subjected to variable expression due to integration-position effects. They allow the integration of very foreign DNA without host range limitations. The telomere opt. contains variant repeats of CTCTRAA. The telomere is pref. the pAt14 plasmid (ATCC 67577). (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant DNA contg. eukaryotic telomere esp. from higher plant useful as vector for specific genes and maintained in nucleus as independent replicating molecule.
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                     Telomere; Arabidopsis thaliana; vector; artificial chromosomes;
                                                                                                                           . 0
                                                                                              100.0%; Score 6; DB 8; Length 6; 100.0%; Pred. No. 7e+08; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 6; DB 1; Length 7; 100.0%; Pred. No. 6e+08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                        Sequence 6 BP; 2 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                relomere of Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 28; Page 50; 65pp; English.
                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-00172467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                89WO-US000795.
                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                               AAN91439 standard; DNA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEHO ) GEN HOSPITAL CORP
                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ausubel FM;
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                                                                                                          Local Similarity
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6 TTAGGG 1
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                                                                                                                                              1 TTAGGG
                                                                                                                                                                                                                                                                                                                                                    tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                              27-FEB-1989;
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                                                                                                                                                                                                                                                                            25-MAR-2003
22-FEB-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richards E,
                                                                                                                                                                                                                                                                                                                                                                                                                        05-0CT-1989
                                                                                                                                                                                                                                                     AAN91439;
                                                                                                Query Match
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                                                                                                                                                                                                                  AAN91439/c
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                  Variant telomere; Arabidopsis thaliana; vector; artificial chromosomes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The DNA is a variant of the telomere of the pAtT4 plasmid (ATCC 67577). (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant DNA contg, eukaryotic telomere esp. from higher plant useful as vector for specific genes and maintained in nucleus as independent replicating molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 6; DB 1; Length 7; 100.0%; Pred. No. 6e+08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7 BP; 3 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                Variant of Arabidopsis thaliana telomere.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                   BP.
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Best Local Similarity 100.v.
                                                                                                                                                                                                                                                            (first entry)
AAN91442/c
ID AAN91442 standard; DNA; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ausubel FM;
                                                                                                                                                                                                                 (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1989-309497/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TTAGGG 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-1989;
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                                                                                                                                                                                                         25-MAR-2003
22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richards E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
19-0CT-1995
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                                                                                                                            AAN91442;
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New peptide nucleic acid (PNA) oligomers are provided which (a) consist of naturally occurring nucleobases covalently bound to a polyamide backbone and (b) hybridise to the translation initiation Aug region, 5' contranslated region (3' UTR), splice curranslated region (3' UTR), splice curranslated region (3' UTR), splice curranslated business of a be used to target chosen from env, gag, pol, rev and tat. The PNAs can be used to target consen from moieties. They have utility as gene-targetted drugs for regulation moieties. They have utility as gene-targetted drugs for modulating HIV processes. Hence they can be used to treat AIDS and other contral infections. They are also useful in diagnostic applications and as research tools. PNA oligomers have high affinity for complementary single stranded DNA. They are also able to form triple helices in which a first or stranded DNA. They are also able to form triple helices in which a first pNA strand binds with the first pNA strand. The PNAs possess no significant charge and are water soluble, which facilitates cellular contake. Further, since they contain amides of non-biological amino acids, they are biostable and resistant to enzymatic degradation by proteases. The present sequence is a specifically claimed PNA sequence (represented by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-
being formed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue"
                                                                                                                                                                                                                                                                                                                                                 Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid sub:unit - binds in complementary manner to DNA and RNA, and useful for modulating HIV viral activity, e.g. in treating AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide nucleic acid 14, targeted to mammalian telomerase.
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                                                                                                                                                                                                                                          (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                   WPI; 1995-082179/11.
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Best Local Similarity
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modified base
                                                                                       WO9504068-A1
                                                                                                                                                                                                    29-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer; inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia; AIDS; HIV; fungal infection; forensic identification; detect; tumour; paternity testing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide nucleic acids hybridising to mammalian telomerase RNA - used to inhibit telomerase, for treating tumours and other proliferative diseases, also for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "Peptide nucleic acid molecule, where N-(2-
aminoethyl)glycine units are linked to nucleotide bases
via glycine amino N through a methylenecarbonyl linker"
   /note= "Sugar-phosphate backbone has been replaced by
peptide backbone"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                     Piatyszek MA, Corey D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                        Shay JW, Wright WE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-512647/47.
                                                                                                                                                                                                                                                                                                                                                               (GERO-) GERON CORP.
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Best Local Similarity
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TTAGGG 7
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                                                                                                                       WO9738013-A1
                                                                                                                                                                               16-OCT-1997.
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96US-00630019

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09-APR-1996;
  Wright WE,
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Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 U; 0 Other; Query Match Best Local Similarity Matches

AAA37572/c RESULT 13

AAA37572;

PNA sequence #30 used to inhibit telomerase activity.

Synthetic

The present sequence represents a peptide nucleic acid molecule which the present sequence represents a peptide nucleic acid molecule which hybridises to the mRNA component of mammalian telomerase, and inhibits telenarase activity. Telomerase is a ribonucleoprotein enzyme that component activity. Telomerase is a ribonucleoprotein enzyme that invented strands of the telomeric DNA, using as a template an 11 invention relates to PNA molecules having a sequence of no more than 25 comesses, which include the sequence GTTAGG. The uncharged nature of the PNA increases the melting temperature of associating strands, increases the rate of association with targeted nucleic acids, and affords greater resistance of degradation by proteases or nucleases. The cancers, neophasia, hyperplasia, neurodegenerative diseases, and other contains and associated pathologies, fungal infections, and other contains and associated pathologies, fungal infections, and other cyctoxic or diseases characterized by abnormal telomera metabolism or telomerase custivity, in combination with antineoplastic and other cyctoxic or cytostatic agents, antifungal agents, and other nucleotides. PNAs may be used for molecular diagnostics, labelled PNAs are used as hybridization probes to detect or quantitate polynucleotides having a human telomerase of telomerase and as not individuals, e.g. paternity testing, based on hTR gene restriction of individuals, e.g. paternity testing, based on hTR gene restriction continity testing, based on hTR gene restriction allows cancerous conditions to be detected with increase and as inhibitors of telomerase activity. The method of the present invention allows cancerous conditions to be detected with increased confidence and possibly at an earlier stage, before cells are detected as cancerous conditions to be detected with increase and man telomerase activity. The method of the present invention can be used to detect an immortal or neophastic cell or tumour tissue or cancer of any origin, provided the New peptide nucleic acid (PNA) compounds that inhibit telomerase activity in mammalian cells is useful as probes to detect the RNA component of a Corey DR; Norton JC, Shay JW, Claim 6; Col 71; 45pp; English. (TEXA ) UNIV TEXAS SYSTEM Piatyszek MA, mammalian telomerase. WPI; 2000-292432/25.

; 0 100.0%; Score 6; DB 3; Length 8; 100.0%; Pred. No. 5.2e+08; ive 0; Mismatches 0; Indels 6; Conservative

0

Gaps

AAA37572 standard; DNA; 8 BP. L5-AUG-2000 (first entry) 

Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer; inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia; AIDS; HIV; fungal infection; forensic identification; detect; tumour; paternity testing; ss.

AAS15436 standard; DNA; 8 BP.

AAS15436 ID AAS1 XX

The Present sequence teptresents a prepride incretc actu molecule which the present sequence teptresents a ribonucleoptotein enzyme that telomerase activity. Telomerase is a ribonucleoptotein enzyme that telomerase activity. Telomerase is a ribonucleoptotein enzyme that telomerase schift is a ribonucleoptotein enzyme that telomerase schift is a ribonucleoptotein enzyme that inclocting expense to PNA molecules having a sequence of no more than 25 bases, which include the sequence GTTAGG. The uncharged nature of the PNA increases the rate of association with targeted muclein strands, increases the rate of association with targeted mucleic acids, and therapeutic PNAs may be used for treating diseases or nucleases. The therapeutic PNAs may be used for treating diseases or nucleases. The therapeutic PNAs may be used for treating diseases or nucleases. The therapeutic PNAs may be used for treating diseases or nucleases. The therapeutic PNAs may be used for treating diseases, aging, human associated pathologies, fungal infections, and other cyctotoxic or syndrome) and associated pathologies, fungal infections, and other vyctotoxic or syndrome) and associated pathologies, fungal infections, and other cyctotoxic or cytosestic agents, antifungal agents, and other nucleotides. PNAs may be cytosestic agents, antifungal agents, and other nucleotides. PNAs may be used for molecular diagnostics, labelled PNAs are also useful as trobes to detect the RNA romponent of a mammalian telomerase and as inhibitors of telomerase activity. The method of the present invention and because of entraperation and propersect or nethods of the present invention can be used to detected as cancerus conditions to be detected with increased confidence and propersect cell expresses telomerase activity and its RNA component. ·. activity /note= "Peptide nucleic acid molecule, where N-(2-aminoethyl)glycine units are linked to nucleotide bases via glycine amino N through a methylenecarbonyl linker" New peptide nucleic acid (PNA) compounds that inhibit telomerase activit in mammalian cells is useful as probes to detect the RNA component of a present sequence represents a peptide nucleic acid molecule which Gaps ö Corey DR; 0; Indels 100.0%; Score 6; DB 3; Length 8; 100.0%; Pred. No. 5.2e+08; Shay JW, Norton JC, Sequence 8 BP; 3 A; 4 C; 0 G; 1 T; 0 U; 0 Other; 0; Mismatches Location/Qualifiers Example 2; Col 33; 45pp; English. 97US-00838545. 96US-00630019. (TEXA ) UNIV TEXAS SYSTEM. Wright WE, Piatyszek MA, Conservative /\*tag= mammalian telomerase. WPI; 2000-292432/25. Local Similarity 1 TTAGGG 6 09-APR-1997; misc feature 09-APR-1996; US6046307-A. 04-APR-2000 Query Match Best Loca Matches RESULT 14

AAS15436; 

(first entry) 14-FEB-2002 PNA 28 inhibiting human and mammalian telomerase activity.

Mammalian; peptide nucleic acid; probe; forensic; paternity testing; human telomerase RNA component; hTR gene RFLP pattern; cancer; inflammation; lymphoproliferative disease; autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS; human immunodeficiency virue; acquired immunodeficiency sydrome; telomere metabolism; mutant; cytostatic; anti-inflammatory; immunosuppressive; polyamide backbone; ss.

sapiens Homo

Synthetic.

Location/Qualifiers Key modified\_base

/\*tag= a /note= "This sequence is a peptide nucleic acid, i.e. i contains a polyamide backbone instead of a deoxyribose backbone"

US6294650-B1

25-SEP-2001

99US-00349532. 08-JUL-1999;

96US-00630019 97US-00838545 09-APR-1996; 09-APR-1997;

(TEXA ) UNIV TEXAS SYSTEM.

Corey DR, Norton JC; Wright WE, Piatyszek MA, Shay JW,

WPI; 2001-638024/73

New peptide nucleic acids that hybridizes to the RNA component of mammalian telomerase, useful for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases.

Claim 7; Col 73; 46pp; English.

The present invention relates to peptide nucleic acids (PNAs), comprising a sequence of 6-25 nucleobases, that inhibit telomerase activity in mammalian cells by hybridising to the RNA component of mammalian telomerase and as inhibit tors of telomerase activity, or to detect and/or quantitate polynucleoride having the human telomerase RNA component (HTR) sequence, as well as in forensic identification of individuals, such as paternity testing or identification of criminal suspects or unknown descendants based on the HTR gene RFLP pattern. The suspects or unknown descendants based on the hTR gene RFLP pattern. The lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases. The PNAs in combination with other pharmaceuticals (such as antineoplastic or cytostatic agents) can be used for treating neoplassic, human immunodeficiency virus (HIV) infections, acquired immunodeficiency syndrome (AIDS) and associated pathologies, and other diseases characterised by abnormal telomere metabolism or telomerase the contract of the con sequence represents one of the PNA sequences of the activity. The present

Sequence 8 BP; 1 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Gaps .; 0 100.0%; Score 6; DB 4; Length 8; 100.0%; Pred. No. 5.2e+08; Live 0; Mismatches 0; Indels Conservative Query Match Best Local Similarity Matches 6; Conserv

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TIAGGG 7

RESULT 15 AAS15474

AAS15474 standard; DNA; 8 BP.

AAS15474;

(first entry) 14-FEB-2002 PNA 34 inhibiting human and mammalian telomerase activity.

Mammalian; peptide nucleic acid; probe; forensic; paternity testing; human telomerase RNA component; hTR gene RFLP pattern; cancer; inflammation; lymphoproliferative disease; autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS; human immunodeficiency virus; acquired immunodeficiency syndrome; telomere metabolism; mutant; cytostatic; anti-inflammatory; immunosuppressive; polyamide backbone; ss.

Homo sapiens. Synthetic. Location/Qualifiers modified base

/\*tag= a /note= "This sequence is a peptide nucleic acid, i.e. i contains a polyamide backbone instead of a deoxyribose backbone"

modified base

/\*tag= b /note= "N= 1-50 peptide nucleic acid nucleobases, selected from U, T, A, G, C or i"

modified base

/note= "N= 1-50 peptide nucleic acid nucleobases, selected from U, T, A, G, C or i" \*tag= c note= "N=

US6294650-B1

25-SEP-2001

99US-00349532. 08-JUL-1999; 

96US-00630019. 97US-00838545 09-APR-1997; 09-APR-1996;

(TEXA ) UNIV TEXAS SYSTEM

Norton JC; Corey DR, Piatyszek MA, Shay JW, Wright WE,

WPI; 2001-638024/73.

orNew peptide nucleic acids that hybridizes to the RNA component of mammalian telomerase, useful for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases.

Disclosure; Col 59; 46pp; English.

The present invention relates to peptide nucleic acids (PNAs), comprising a sequence of 6-25 nucleobases, that inhibit telomerase activity in mammalian cells by hybridising to the RNA component of mammalian cells by hybridising to the RNA component of mammalian telomerase and as inhibitors of telomerase activity, or to detect and/or quantitate polynucleotide having the human telomerase RNA component (hTR) sequence, as well as in forensic identification of individuals, such as paternity testing or identification of criminal suspects or unknown descendants based on the hTR propertion of lumpar can be further used for treating or preventing cancer, inflammation, lymphoproliferative diseases, autoimmune disease, or neurodegenerative diseases. The PNAs in combination with other pharmaceuticals (such as

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TTAGGG 6

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antineoplastic or cytostatic agents) can be used for treating neoplasia, byperplasia, human immunodeficiency virus (HIV) infections, acquired immunodeficiency syndrome (AIDS) and associated pathologies, and other CC diseases characterised by abnormal telomera metabolism or telomerase activity. The present sequence represents one of the PNA sequences of the CC invention. Note: The present sequence is given in the SRQ ID listing but XX
SQ Sequence 8 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 2 Other:
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SQ Sequence 8 BP; 1 A; 0 C; 3 G; 2 T; 0 U; 2 Other;

Query Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 8;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTAGGG 6

1 TTAGGG 6 |||||| 2 TTAGGG 7

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Search completed: August 11, 2004, 17:56:37 Job time: 89.043 secs

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Sequence 49, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 11, Appli
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Sequence 49, Appl
                                                                                                                                                         August 11, 2004, 19:00:04; Search time 86.5161 Seconds (without alignments) 340.279 Million cell updates/sec
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Sequence 1,
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11. Capt2 6/ptodata/2/pubpna/US07 PUBCOMB.seq: *

12. (cgn2 6/ptodata/2/pubpna/DS07 NEW PUB.seq: *

13. (cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq: *

14. (cgn2 6/ptodata/2/pubpna/US06 PUBCOMB.seq: *

15. (cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq: *

16. (cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq: *

17. (cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq: *

18. (cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq: *

19. (cgn2 6/ptodata/2/pubpna/US08 PUBCOMB.seq: *

19. (cgn2 6/ptodata/2/pubpna/US09 PUBCOMB.seq: *

10. (cgn2 6/ptodata/2/pubpna/US09 PUBCOMB.seq: *

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10. (cgn2 6/ptodata/2/pubpna/US09 NEW PUB.seq: *

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10. (cgn2 6/pt
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-940-173A-1
US-01-122-630-12
US-10-122-633-11
US-10-122-633-12
US-10-255-53-12
US-10-336-265-3
US-10-336-265-3
US-10-336-265-4
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US-09-735-363A-49
US-09-730-893-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA:*
                                                                                                       - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listing first 45 summaries
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Match Length
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seq length: 200
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1121...
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1161...
1191...
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Maximum DB s
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US-09-817-387-29

Sequence 64, A	Sequence 9, Apr	Sequence 27, Ar	س	~	Sequence 13. Ar	-	Semience 16. Ar	Sequence 6. Appl	Segmence 6. Apr	Sequence 4. Ann	Sequence 4. Apr	Sequence 58. Ar	Segmence 19. Apr	Semience 527	Sequence 56. Ar	Seguence 358. A	Sequence 613. A	Sequence 1694.	Sequence 294. A	Sequence 294, A	Sequence 41, Ap	Sequence 92, Ap		Sequence 1297,		Segmence 1439	Sequence 41. An	Segmence 2. Appl	Sequence 63. An	Sequence 57, Ap	
			US-10-382-754B-3			US-10-705-531-15		ב	US-09-940-173A-6	US-09-730-893-4	US-09-940-173A-4	US-10-336-265-58	US-09-728-574-19	US-10-325-810-527	US-10-033-145-56	US-10-033-145-358	US-10-033-145-613	US-10-033-145-1694	US-10-044-692-294						US-10-330-627-1298	US-10-330-627-1439	US-10-434-479-41	US-09-057-351-2	US-09-835-370-63	US-09-249-155-57	
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6 100.0	•								100.0	100.0	100.0	6 100.0	100.0	100.0	100.0	100.0	100.0	100.0	6 100.0 10			6 100.0 10					6 100.0 10	Г	6 100.0 11	6 100.0 13	
15	P 1	C 17	18	19	20	21	22	23	24	25	26	27	c 28	29	30	31	32	33	34	35	36	m)	C 38	99 0	4	41	42	c 43	44	c 45	

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## ALIGNMENTS

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Gaps
Sequence 29, Application US/09817387
Sequence 29, Application US/09817387
Sequence 29, Application US/09817387
Sequence 20, Application US/09817387
GENERAL INFORMATION
TITLE OF INVENTION: Chimeric Oligonuclectides and the Use Thereof
FILE REFERENCE: 101195-24
CURRENT APPLICATION UNMBER: US/09/817,387
CURRENT FILING DATE: 2001-23-26
PRIOR FILING DATE: 1997-05-02
PRIOR FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                         Description of Artificial Sequence: telomeric DNA of man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 6; DB 9; Length 6; 100.0%; Pred. No. 7.9e+08; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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TTAGGG 6
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US-09-735-363A-49
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Sequence 2, Application US/09907279;
Sequence 2, Application US/09907279;
Publication No. US20020068296A1
GENERAL INFORMATION:
APPLICANT: Heller, Adam
TITLE OF INVENTION: CATHODIC PROTECTION OF NUCLEIC ACID SEQUENCES
FILE REPERENCE: 11154.41USU1
CURRENT FILIAG DATE: 2001-07-17
CURRENT FILIAG DATE: 2000-07-17
PRIOR APPLICATION NUMBER: US 60/218,959
PRIOR PILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Primer US-09-940-173A-1
  APPLICANT: SALAZER, MIGUEL
APPLICANT: HURLEY, LAURENCE H.
TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A
TITLE OF INVENTION: G-OUADRUPLEX-INTERACTION COMPOUND
FILE REFERENCE: UTSB:679USD2
CURRENT PERLICATION NUMBER: US/09/940,173A
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/730,893
RRIOR FILING DATE: 1909-04-02
PRIOR APPLICATION NUMBER: 60/073,629
PRIOR APPLICATION NUMBER: 60/073,629
PRIOR PILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-02
PRIOR SEQ ID NOS: 12
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 6; DB 10; Length 6; 100.0%; Pred. No. 7.9e+08;
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US-09-907-279-2
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100.0%; Pred. No. 7.9e+08;
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Publication No. US20030032610A1
GENERAL INPORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Fller, Mark S.
APPLICANT: Yaar, Mina
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Best Local Similarity 100.
Matches 6; Conservative
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Matches 6; Conserv
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              APPLICANT: Phillip, Nigel
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
FILE REFERENCE: 02811-0181
CURRENT APPLICATION NUMBER: US/09/735,363A
CURRENT FILING DATE: 2000-12-12
PRIOR FILING DATE: 1999-12-13
PRIOR FILING DATE: 1999-12-13
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Primer US-09-730-893-1
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Patent No. US20020107258A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FEDOROFF, OLEG Y.
APPLICANT: SALAZAR, MIGHES H.
TITLE OF INVENTION: INHIBITION OF HUMAN TELOMERASE BY A TITLE OF INVENTION: G-QUADRUPLEX-INTERACTION COMPOUND; FILE REFERENCE: USE-6790CF; CURRENT APPLICANTON NUMBER: US/09/730,893; CURRENT APPLICATION NUMBER: US/09/730,893
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100.0%; Score 6; DB 9; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.9e+08;

Matches 6; Conservative 0; Mismatches 0; Indels
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CTHER INFORMATION: Synthetic Oligonucleotide
US-09-735-363A-49
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PRIOR APPLICATION NUMBER: 09/244,675
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: 60/073,629
PRIOR FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PATENTI VEY: 2.1
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ORGANISM: Artificial Sequence
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APPLICANT: Filion, Mario
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Best Local Similarity
Matches 6; Conserv
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US-09-940-173A-1
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US-09-730-893-1
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; Sequence 1, Application US/09940173A; Publication No. US20030040525A1; GENERAL INFORMATION:

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APPLICANT: KERWIN, SEAN M

Length 6; Indels

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                                                                                                     Sequence 11, Application US/10122633

Publication No. US20030032611A1

GENERAL INFORMATION;
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Taar, Mina
TITLE OF INVENTION: Oligomuclectides
FILE REFERENCE: 0064.1088-019
CURRENT APPLICANTON: WOMBER: US/10/122,633
CURRENT APPLICATION NUMBER: US 09/540,843

PRIOR APPLICATION NUMBER: US 09/540,843

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 11

SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6;
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APPLICANT: Glichrest, Mark S.
APPLICANT: Glichrest, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054.1088-019
CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
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100.0%; Pred. No. 7.9e+08;
iive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/10122633 Publication No. US20030032611A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 6; Conservative
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                   6 TTAGGG 1
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TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REPERENCE: 0654-1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-06
PRIOR FILING DATE: 1995-06-03
PRIOR FILING DATE: 1996-06-03
PRIOR FILING DATE: 1996-06-03
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PASLSEQ for Windows Version 4.0
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APPLICANT: Eller, Mark S.

APPLICANT: Eller, Mark S.

APPLICANT: Eller, Mark S.

TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonucleotides

TITLE OF INVENTION: Oligonucleotides

TITLE REPERENCE: 0054.1088-018

CURRENT FILING DATE: 1002-04-12.

PRIOR APPLICATION NUMBER: US/10/122,630

CURRENT FILING DATE: 1995-06-06

PRIOR APPLICATION NUMBER: PCT/US96/08386

PRIOR FILING DATE: 1996-0-03

PRIOR FILING DATE: 1996-0-03

PRIOR FILING DATE: 1996-0-03

PRIOR FILING DATE: 2000-03-11

PRIOR FILING DATE: 2000-03-11

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 12
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100.0%; Score 6; DB 15; I
Best Local Similarity 100.0%; Pred. No. 7.9e+08;
Matches 6; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100..
6; Conservative
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GENERAL INFORMATION:

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Sequence 63, Application US/10336265
Publication No. US20030148988A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: The Elongation of Telomere Repeats
TITLE OF INVENTION: the Elongation of Telomere Repeats
TITLE OF INVENTION: the Elongation of Telomere Repeats
CURRENT PRINCATION NUMBER: US/10/336,265
CURRENT PRINCATION NUMBER: US 60/345,056
PRIOR PRILING DATE: 2002-01-04
NUMBER OF SEQ ID NOS: 64
APPLICANT: Kool, Eric T.
TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: the Elongation of Telomere Repeats
FILE REPERBENCE: 12665.0021.NPUS01
CURRENT APPLICATION NUMBER: US/10/336,265
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: US 60/345,056
PRIOR FILING DATE: 2002-01-04
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.2
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US-10-336-265-4/c
US-10-336-265-4/c
sequence 4, Application US/10336265
publication No. USZ0030148988A1
GENERAL INFORMATION:
TITLE OF INVENTION: Telcomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: the Elongation of Telomere Repeats
FILE REFRENCE: 12565.0021.NPUS01
FILE REFRENCE: 12565.0021.NPUS01
CURRENT APPLICATION NUMBER: US/10/336,265
CURRENT APPLICATION NUMBER: US 60/345,056
PRIOR APPLICATION NUMBER: US 60/345,056
PRIOR PILING DATE: 2002-01-04
NUMBER OF SEQ ID NOS: 64
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Best Local Similarity luv...
Lag 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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US-10-336-265-63
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APPLICANT: Kool, Eric T.
TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: the Blongation of Telomere Repeats
FILE REFERENCE: 12665.0021.NPUS01
CURRENT PAPLICATION NUMBER: US/10/336,265
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: US 60/345,056
PRIOR FILING DATE: 2002-01-04
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                   APPLICANT: Gryanov, Sergei
APPLICANT: Gryanov, Sergei
APPLICANT: Pongracz, Kristlina
APPLICANT: Tolman, Richard L.
APPLICANT: Tolman, Richard L.
APPLICANT: Morin, Gregg B.
TITLE OF INVENTION: Oligonucleotide Conjugates
FILE REFERENCE: 072/002P
CURRENT APPLICATION NUMBER: US/10/255,535
CURRENT FILING DATE: 2002-09-25
PRIOR PILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/278,322
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 8
LENGTH: 6
LENGTH: 6
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Publication No. US20030148988A1
                                                                                       ; Sequence 8, Application US/1025535; Publication No. US20030138814A1; GENERAL INFORMATION: APPLICANT: Geron Corporation
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RESULT 15
US-10-336-265-64

i Sequence 64, Application US/10336265

j Education No. US20030148988A1

i CENERAL INFORMATION:

TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION: Telomere-Encoding Synthetic DNA Nanocircles, and their use for TITLE OF INVENTION WUMBER: US_001.N9US01

CURRENT FILING DATE: 2003-01-03

PRIOR PELLING DATE: 2002-01-04

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PatentIn version 3.2

LENGTH: EINGTH: 6
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Best Local Similarity 66.7%; Pred. No. 7.9e+08;
Matches 4; Conservative 2; Mismatches 0; Indels
; TYPE: DNA; ORGANISM: Homo sapiens US-10-336-265-63
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CORGANISM: Homo sapiens
US-10-336-265-64
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AW248958 2819454.3
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AZ82673 BQ59348 AZ34551 AZ62717 AZ66290	AZ96000 AZ96000 TA158A0 TA199G0 AW24883 AW24883 CF28181	2 2 4 3 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	AZ877213 AA527213 D13245 AZ3245 AZ46464 AZ4683332 AZ500411	AZ62950 AZ66664 AZ8510 AZ8510 AZ85510 AZ62381 AZ45281 AZ62397 AZ62397 AZ62397 AZ62397 AZ62397 AZ62397
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ALIGNMENTS

AW248958 16 bp mRNA linear BST 07-JAN-2000 2819454.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819454 3', Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LiNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LiML at:
www-bio.lln.gov/bbrp/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center
Trimming: cross\_match from University of Washingtion Genome Center Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.

1 (Joses 1 to 16)

NIH-MGC http://mgc.nci.nih.gov/.

NAtional Institutes of Health, Mammalian Gene Collection (MGC)

Other ESTS: 2819454.5prime
Contact: Robert Strausberg, Ph.D. AW248958.1 GI:6591951 Homo sapiens (human) mRNA sequence. sapiens AW24895 Homo DEFINITION ORGANISM AUTHORS TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS SOURCE RESULT 1 AW248958 REFERENCE

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High quality sequence stop: 19.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musing Burbers 1 to 19)

Sunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R. Dingey,A., von Diasmid inserts

I Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
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/clone="MAGB: 2819454"

/tissue_type="mall cell carcinoma"

/clone_lib="MGC3"

/lab_host="MGC3"

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1M0154G12R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0154G12 R, genomic survey sequence.
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washingtion Genome Center: http://www.ashington.edu Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.
Plate: LLCMI row: K column: 7 Plate: LLCMI row: K column: 7 Plate: LLCMI row: K column: 7 Plate: LCMI row: Column: 7 Plate: LCMI row: K c
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Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGGAAACAGCTATGACC
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High quality sequence stop: 19.
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/db_xref="taxon:9606"
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Fax: 801 585 7177
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(http://www.jax.org/resources/localcury mouse punk resource that the the theory as a very resource documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligomuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pw042 (gil 4732114|gb|AR129072.1), a copy.number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouses DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xiilo-Gold (Stratagene) cells and selected for ampicillin resistance."
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Bukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (Dases I to 19)
S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausenn,A. and Wright,D.,Weiss,R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unyublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah Genome Center
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                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0200 row: F column: 10
Seq primer: CACACAGGAAACAGCTAATGACC
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                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC1M0154G12"
Location/Qualifiers
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us-09-540-843-11.szlm200.rst

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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Insert Length: 10000 Std Error: 0.00
Plate: 0102 row: N column: 07
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Fax: 801 585 7177
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Unpublished (2000)
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1M0443A17R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0443A17 R, genomic survey sequence.
                                                                                                                                                                                 /lab host="B. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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                                            'organism="Mus musculus"
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University of Utah Genome Center
University of Utah
                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0200F10"
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Location/Qualifiers
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                                                                                                                                                                   sex="Male'
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Fax: 801 585 7177
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LOCUS
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  FEATURES
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Induction C./ Water D. Water D
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2M0102N07R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZW0102N07 R, genomic survey sequence.
AZ826736
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Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clome_lib="Mouse_lokb plasmid UGGZN library"
/note="Vector: PWD4zny, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                      organism="Mus musculus"
                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UUGC1M0443A17"
Location/Qualifiers
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source

FEATURES

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AZ345513 20 bp DNA linear GSS 29-SEP-2000 1M0080J04F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0080J04 F, genomic survey sequence.
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                       /clone lib="MPIZ-ADIS-024-developing root"
/note="Wector: pCMWSPORT6; Site 1: Sal1; Site 2: Not1;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sal1-Not1, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                      SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. L (bases 1 to 20).

Dunn, D., Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
                        "mol type="mRNA"
'cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
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                                                                                                         | db xref="GABI:193369"
| db xref="taxon:161934"
| clone="024-026-P04"
| Lissue_type="developing root"
| lab_host="EMDH10B"
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Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: J column: 04
organism="Beta vulgaris"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0080J04"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWaD42 (gil #732114 [gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent B. coli X110-Gold (Stratagene) cells and selected for ampicillin resistance."
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Beta vulgaris
Beta vulgaris
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 20)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
and Radelof,U.
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                                                                                                                                                                                                                            /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UNGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson
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ADIS DNA core facility at MPIZ
MAx-Planck-Institute for Plant Breeding Research
Max-Panck-Institute for Plant Breeding Research
Fax: 0.492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 20 Std Brror: 0.00
Plate: 26 row: P column: 04
Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
Location/Qualifiers
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                                                         organism="Mus musculus"
                                                                                    mol_type="genomic DNA"
strain="C57BL/6J"
                                                                                                                                             db xref="taxon:10090"
                                                                                                                                                                     clone="UUGC2M0102N07"
location/Qualifiers
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BQ593485.1 GI:26123068
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Best Local Similarity 100.

Matches 6; Conservative
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BQ593485/c LOCUS

RESULT 6

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ORIGIN

SOURCE ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS source

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                                                                                             (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pm/2 (gil 47321141gb] AR129072.1), a copy-number of pm/2 (gil 47321141gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (Dases 1 to 20)

S Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah

Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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Insert Length: 10000 Std Error: 0.00
                                                                                  Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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/mol type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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Plate: 0467 row: 0 c
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Fax: 801 585 7177
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/clone_lib="Mouse_10kb_plasmid_UUGC1M_library"
/note="Vector: PWD42nv; Purified genomic_DNA_from_M.
musculus_C57BL/6J (male) was obtained_from_the_Jackson
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100.0%; Pred. No. 1.2e+06;
iive 0; Mismatches 0;
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC1M0542G17"
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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Mus musculus
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                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide Kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 47421141gb] AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0.0601d (Stratagene) cells and selected for ampicillin resistance."
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S. Unan,D., Aoyadi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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                                                                  Laboratory Mouse DNA Resource
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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/strain="C57BL/6J"
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil 47321141gb) AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. ond transformed into chemically-competent E. and transformed into adaptored for ampicillin resistance."
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
/clone_lib="Mouse 10kb plasmid_UUGCIM_library"
/note="Vector: PWD42nv; Purified_genomic_DNA_from M.
musculus C57BL/6J (male) was obtained_from the Jackson
Laboratory Mouse_DNA_Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 48412, USA 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
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Insert Length: 10000 Std Error: (
Plate: 0227 row: G column: 21
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="UUGC2M0227G21"
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Location/Qualifiers
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Unpublished (2000)
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Homo sapiens (human)
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                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nh1@sanger.ac.uk
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Best Local Similarity
Matches 6; Conserv
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Query Match
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Matches 6; Conserv
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TA199G02Q/c
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SOURCE
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                                                                                   (http://www.jax.org/resources/
(http://www.jax.org/resources/
(http://www.jax.org/resources/
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligomucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWnp(2 (gil 4732114)gb]AFL29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma bruce; (TREU927/4 GUTAT 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Vener, J.C. (Maxing small insert libraries for whole genome shotgun sequencing small enome Sequencing: A practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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Details of T. bruce; sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CBl0 1SA, B-mail: barrell@sanger.ac.uk and
/clone_lib="Mouse_10kb_plasmid_UUGC2M_library"
/note="Vector: PWD42nv; Purified genomic_DNA_from_M.
musculus_C57BL/6J (female) was obtained_from_the_Jackson
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Trypanosoma brucei
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                              aboratory Mouse DNA Resource
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/strain="TREU927"
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/clone="158a03"
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2821056.3prime NIH_MGC_7 Homo sapiens CDNA clone IMAGE:2821056 3',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 21)
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Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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T. brucei sheared genomic DNA clone 199g02, reverse sequence,
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/strain="TREU927"
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/clone="199g02"
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                                                   Dipublished (1999)

Other ESTS: 2821056.5prime

Other ESTS: 2821056.5prime

Contact: Robert Straubberg, Ph.D.

Email: cgapbs-rømail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/Ling at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Screes: PHRED from University of Washingtion Genome Center.

Trimming: cross_match from University of Washingtion Genome Center.

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Trimming: cross_match from University of Washingtion Genome Center.

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Trimming cross_match from University of Washingtion Genome Center.

PHRAP suite. Poly-T identification: patMatch.pl from Berkeley

Trimming vertor sequence. Trace file contained 21 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the

presence of a XhoI site followed by a run of 14 or more T residues

poly-denylation.
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/clone="INAGB: 2821056"

/tissue type="small cell carcinoma"

/clone lib="McG3"

/lab host="McG3"

/clone lib="NIH MGC 7"

/clone lib="NIH MGC 7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhOI; Site 2:

ECORI; CDNA made by oligo-dr priming. Directionally

cloned into ECORIXADO sites using the following 5;

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-CDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."
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2821108.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821108 3',
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I (bases 1 to 21)
III (bases 1 to 21)
III MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_ESTS: 2821108.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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6; Conservative 0; Mismatches n. Thall
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High quality sequence stop: 21.
Location/Qualifiers
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/db_xref="taxon:9606"
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Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washingtion Genome Center. Vector
Trimming: cross_match from University of Washingtion Genome Center.
PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
brosophila Genome Project. University of Washingtion Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 10
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 21 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
polyadenylated.
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/ab_nost="DH10B (phage-resistant)"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2821108"
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Name
t score: 20  g table: 10ENTITY_NUC  dapop 10.0, Gapext 1.0  ed: 3470272 seqs, 21671516995 residues  number of hits satisfying chosen parameters:  m DB seq length: 200  mxximum Match 00%  mxximum Match 100%  in gb ba:* 2: gb hg:* 3: gb hg:* 4: gb co:* 11: gb ba:* 5: gb pr:* 11: gb pr:* 11: gb st:* 12: gb ro:* 11: gb st:* 12: gb ro:* 13: gb vi:* 13: gb vi:* 14: gb vi:* 15: em fun:* 16: em fun:* 17: em hun:* 18: em ph:* 18: em ph:* 22: em pv:* 23: em ph:* 24: em ph:* 25: em ph:* 25: em ph:* 26: em ro:* 27: em fun:* 28: em htg inv:* 29: em htg ph:* 21: em htg ph:* 22: em htg ph:* 23: em htg ro:* 24: em ro:* 25: em ro:* 25: em ro:* 26: em ro:* 27: em ro:* 27: em ro:* 28: em ro:* 28: em ro:* 28: em ro:* 29: em ro:* 20: em ro:* 20:
rable: IDENTITY_NUC  Gapop 10.0 , Gapext 1.0  mber of hits satisfying chosen parameters:  DB seq length: 200  Cessing: Minimum Match 100%  Listing first 45 summaries  GenEmbl: *  1: 9b ba: *  2: 9b ba: *  5: 9b ba: *  6: 9b pat: *  7: 9b pat: *  8: 9b po: *  10: 9b pat: *  10: 9b pat: *  11: 9b pat: *  12: 9b ba: *  13: 9b low: *  10: 9b pat: *  11: 9b sts: *  12: 9b ba: *  13: 9b low: *  14: 9b vi: *  15: em ba: *  16: em hum: *  17: em hum: *  18: em li: *  20: em ow: *  21: em ov: *  22: em ov: *  23: em pat: *  24: em ph: *  25: em pl: *  25: em li: *  26: em ro: *  27: em hug-hum: *  28: em hug-chher: *  31: em hug-dus: *  32: em hug-dus: *  33: em hug-dus: *  34: em hug-wu: *  35: em hug-wu: *  36: em hug-wu: *  37: em hug-wu: *  38: em hug-vrt: *  38: em hug-vrt: *  39: em hug-wu: *  30: em hug-wu: *  40: em hug-wu: *  40: em hug-wu: *  40
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

PAT 29-OCT-2001											
linear											
DNA								Σ,	nts	.,	_
AX268760 20 bp	Sequence 8 from Patent WO0174342. AX268760	AX268760.1 GI:16541832	•	synthetic construct	synthetic construct	artificial sequences.		Gilchrest, B.A., Yaar, M. and Eller, M.	Use of locally applied dna fragments	Patent: WO 0174342-A 8 11-OCT-2001;	TRUSTEES OF BOSTON UNIVERSITY (US)
RESULT 1 AX268760 LOCUS	DEFINITION ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE	JOURNAL	

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BD246071 15.3 bp DNA linear PAT 17-JUL-2003
Development of novel antibiotics based on bacteriophage genomics.
BD246071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHAGETECH INC
OS Staphylococcus aureus bacteriophage 44AHJD
N JP 2002531107-A/806
PD 24-SEP-2002
PF 03-DEC-1999 JP 2000585456
PR 03-DEC-1999 US 60/110992,03-JUN-1999 US 09/326144 PR 01-DEC-1999 US 60/157218 PR 01-DEC-1999 US 60/157218 PR PELLETIER, PHILLIPPE GROS, MICHAEL DUBON
PC C12N15/09, A01N63/00, A61N38/00, A61N45/00, A61P31/04, C07K14/005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C12N1/00,
C12N1/21,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/566, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unclassified.
1 (bases 1 to 153)
Pelletier, J., Gros, P. and Dubow, M.
Development of novel antibiotics based on bacteriophage genomics
Patent: JP 2002531107-A 806 24-SEP-2002;

    120
    organism='Artificial sequences'

                                                                                                                                                                                                                                                                                                                                    Query Match

74.0%; Score 14.8; DB 6; Length 120;
Best Local Similarity 88.9%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels (
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 METHOD FOR DETECTING NUCLEIC ACID
Patent: JP 1994343499-A 4 20-DEC-1994;
CANON INC
                                                                                                                                                                                                                                                    1. .120
/organism="unidentified"
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                         Artificial sequences.
JP 1994343499-A/4
20-DEC-1994
04-JUN-1993 JP 1993134615
                                                                                                                                                                                                                                     Location/Qualifiers
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Location/Qualifiers
                                                                                                                  KATO KINYA
C1201/68;
strandedness: Single;
topology: Linear;
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aureus bacteriophage
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PC C12M1/
PC C12N1/
C12N15/00,
                                              None
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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BD246071/c
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                                                                                                                                                                                                                                                                                                                                               unidentified
unidentified
unidentified
unclassified.
1 (bases 1 to 120)
Kato,K. and Kuriyama,A.
NUCLBIC ACID PROBE AND METHOD FOR DETECTING NUCLEIC ACID
Patent: UP 19943498-A 3 20-DEC-1994;
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/organism='Artificial sequences'.
Location/Qualifiers
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74.0%; Score 14.8; DB 6; Length 120;
Best Local Similarity 88.9%; Pred. No. 5.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels
                                                                                                              ch 100.0%; Score 20; DB 6; Length 20; Similarity 100.0%; Pred. No. 8.9; 20; Conservative 0; Mismatches 0; Indels
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             1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA Fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            topology: Linear;
Location/Qualifiers
                                                                                                                                                                                                                                                                              DNA
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                                                                                                                                                                                                                                                                        Synthetic DNA for probes and primers. B08557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Artificial sequences.
JP 1994343498-A/3
C0-DEC-1994
03-JUN-1993 JP 1993133640
EATO KINYA, KURIYAMA AKIRA
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Location/Qualifiers
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strandedness: Single;
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JP 1994343498-A/3.
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Best Local Similarity
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E08557/c
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E08566/c
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Homo sapiens
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AX909486/c
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PCR conditions="25 ul reaction mix containing 1X buffer,

3 mM MgCl, 2 units of AmpliTaq DNA polymerase Stoffel

fragment (Perkin Elmer), 0.24 mM dNTP, 100 ng primer, and

40 ng template DNA. Amplification was accomplished with 40

cycles of 1 min at 94 C, 1 min at 36 C, and 2 min at 72 C

using the fastest transitions available"
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                                ·.
                                                                                                                                                                            STS 12-JAN-2001
                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Aegilops.
1 (bases 1 to 166)
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                                                                                                                                                                                                                                                                                                                                                                        Sun,L.-H. and Wang,R.R.-C. Identification and sequences of RAPD markers for Aegilops caudata
                                                                                                                                                                            AF025868 12-JAN-20
Aegilops markgrafii RAPD marker generated by Operon primer OP003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="RAPD marker generated by Operon primer OP003; C genome; in the two addition lines derived from the amphiploid of Triticum aestivum X Aegilops caudata"
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                                Gaps
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Sun, L.-H. and Wang, R.R.-C.
Direct Submission
Submitted (20-SEP-1997) FRRL, USDA-ARS, 695 N 1100 E, Logan,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Alicyclobacillaceae.
1 (bases 1 to 178)
Score 14.2; DB 6; Length 153; Pred. No. 1.2e+04;
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                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Aegilops markgrafii"
/mol_type="genomic DNA"
/db_xref="taxon:4494"
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                              0; Mismatches
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1. .166
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                                                                1 GCATGCATGCATTACGTAC 19
                                                                                              70 GCATACCTGCATTACGTTC 52
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M79375.1 GI:173814
16S ribosomal RNA.
1 of 3
                                                                                                                                                                                                       sequence tagged site. AF025868
Query Match 71.0%;
Best Local Similarity 84.2%;
Matches 16; Conservative
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Aegilops markgrafii
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Best Local Similarity 84.27
Matches 16; Conservative
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AF025868
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PAT 17-AUG-2003
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                                                                                                                        Original source text: bacterium ALV (individual_isolate ALV) rRNA.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unclassified.
1 (bases 1 to 162)
Runsch,C.A., Choi,G.H., Barash,S., Dillon,P.J., Fannon,M.R. and
Rosen,C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Olsen,G.J. and Pace,N.R.
Evolutionary relationships among sulfur- and iron-oxidizing
eubacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.0%; Score 13.8; DB 6; Length 162; 88.2%; Pred. No. 2e+04; ive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                    Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus polynucleotides and sequences Patent: US 6593114-A 1694 15-JUL-2003; Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                      Score 14.2; DB 1;
Pred. No. 1.2e+04;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AR355576 1694 from patent US 6593114.
                                                     J. Bacteriol. 174 (1), 269-278 (1992)
92104973
1729214
                                                                                                                                                                                                                                                                                                             /product="16S ribosomal RNA"
                                                                                                                                                                                        organism="bacterium ALV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                       /db_xref="taxon:31975"
1. .178
                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                         /mol_type="rRNA"
/isolate="ALV"
                                                                                                                                                                                                                                                                                            /gene="16S rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 CTTGCATGTATTACGCACG 42
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                                                                                                                                                                                                                                                                                                                                                                      ch 71.0%;
1 Similarity 84.2%;
16; Conservative
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Matches 15; Conservative
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PAT 26-JUL-1995
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    Synthetic insecticidal gene, plants of the genus oryza transformed with the gene, and production thereof Patent: US 5436391-A 34 25-UUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 58)
Fujimoto,H., Ito,K., Yamamoto,M. and Shimamoto,K.
Fyithetic insecticidal gene, plants of the genus oryza transformed with the gene, and production thereof
Patent: US 5436391-A 35_25-UUL-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                   1. .58
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                   0; Mismatches
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/organism="unknown"
/wol_type="unassigned DNA"
                                                                           Location/Qualifiers
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Matches 16; Conserv
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Best Local Similarity
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I (bases I to 196)

Edwards, J. B.D.M., Duclair, E. and Jordan, J.Y.

Sequence tag and encoded human protein

Patent: JP 2001269182-A 21265 02-OCT-2001;
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JP 2001269182-A/21265
02-OCT-2001
24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
                                                                                                                                                                                                                  Gaps
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larity 88.2%; Pred. No. 1.9e+04;
Conservative 0; Mismatches 2; Indels
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Unclassified.
1 (bases 1 to 58)
Fujimoto,H., Ito,K., Yamamoto,M. and Shimamoto,K.
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BD045019
BD045019
JP 20012586761
Homo sapiens (human)
Homo sapiens
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                     1. .196
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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I13500.1 GI:910841
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Best Local Similarity 88.2
Matches 15; Conservative
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Matches 15; Conserv
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PC C12P2
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/organism='Artificial sequences'. Location/Qualifiers
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Location/Qualifiers
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Patent: JP 1994343499-A 5 20-DEC-1994;
             Kato,K.
METHOD FOR DETECTING NUCLEIC ACID
Patent: JP 1994343499-A 5 20-DEC-1994;
CANON INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 י איי יי איי א Synthetic DNA for probe and primer.
B08567

    76
    /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

                                                                                                                                                                                                                                                 1. .76
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 1994343499-A/5
20-DEC-1994
04-JUN-1993 JP 1993134615
KATO KINYA
                                                                           Artificial sequences.
JP 194343499-A/5
20-DEC-1994
KATO KINYA
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strandedness: Single;
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strandedness: Single;
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Best Local Similarity 80.0°
Matches 16; Conservative
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1 (bases 1 to 76)
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(bases 1 to 76)
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                                                                 OCC CC CC CC EFF
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                        unclassified.

1 (bases 1 to 76)

Kato, K. and Kuriyama, A.

NUCLEIC ACID PROBE AND METHOD FOR DETECTING NUCLEIC ACID

Patent: JP 199434498-A 4 20-DEC-1994;

CANON INC
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                         /organism='Artificial sequences'. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 76;
                                                                                                                                Query Match 68.0%; Score 13.6; DB 6; Length 76; Best Local Similarity 80.0%; Pred. No. 2.7e+04; Matches 16; Conservative 0; Mismatches 4; Indels
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80.0%; Pred. No. 2.7e+04;
tive 0; Mismatches 4;
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topology: Linear;
Location/Qualifiers
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Synthetic DNA for probe and primer.
E08567
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                      1. .76
/organism="unidentified"
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/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-DEC-1994
03-JUN-1993 JP 1993133640
KATO KINYA, KURIYAMA AKIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Artificial sequences. JP 1994343498-A/4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GCATGCATGCATTACGTACG 20
                                                                                                                                                                                     1 GCATGCATGCATTACGTACG 20
                                                                                                                                                                                                      53 GCATGCATGCATCGCGCGCG 72
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JP 1994343499-A/5.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                           E08558
E08558.1 GI:2176673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 80.0 nes 16; Conservative
                                                                                                                                                                                                                                                                                                                                   JP 1994343498-A/4.
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unidentified
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E08567
LOCUS
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VERSION
KEYWORDS
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RESULT 13 E08558/c LOCUS

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REFERENCE AUTHORS TITLE JOURNAL

SOURCE

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Thu Aug 12 09:23:32 2004

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1 GCATGCATGCATTACGTACG 20

Search completed: August 11, 2004, 19:31:44 Job time : 1272.68 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

August 11, 2004, 15:32:08; Search time 289.032 Seconds (without alignments) 293.960 Million cell updates/sec Run on:

US-09-540-843-8 20 Title: Perfect score:

1 gcatgcatgcattacgtacg 20 Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY\_NUC Scoring table:

3373863 segs, 2124099041 residues Searched: 3774412 of hits satisfying chosen parameters: Total number

Minimum DB seq length: 0 Maximum DB seq length: 200

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries N\_Geneseq\_29Jan04:\* Database

geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002s:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2004s:\* genesegn1990s:\* genesegn2000s:\* genesedn1980s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Aaz10697 Oligonucl	Aas14912 Melanogen	Acd25827 Melanogen	Acd25777 Oligonucl	Abk91410 Multiple		_	Aaq84038 Plasmid p	Aca23973 Prokaryot	Aaa69048 Bacteriop	Aav76005 Staphyloc	Aac21274 Human sec	Aat29051 Maltogeni		-				_	Aag84037 Plasmid p	Abx91312 Murine ge	Aad19573 Rhizopus	Aac23914 Human sec
ID	AAZ10697	AAS14912	ACD25827	ACD25777	ABK91410	ABK91409	AAQ95093	AAQ84038	ACA23973	AAA69048	AAV76005	AAC21274	AAT29051	AAQ95094	AAQ95094	AAQ84039	AAQ84039	AAQ35972	AAQ95092	AAQ84037	ABX91312	AAD19573	AAC23914
DB	7	4	æ	8	9	9	7	N	7	ო	~	m	7	7	7	7	7	7	~	N	7	Ŋ	'n
% Query Match Length	20	20	20	20	42	42	120	120	141	153	162	196	28	16	16	16	9/	7.0	124				152
% Query Match	100.0	100.0	100.0	100.0	76.0	0.97	74.0	74.0	71.0	71.0	69.0	0.69	68.0	68.0	68.0	68.0	68.0	67.0	67.0	67	67.0	0.99	66.0
Score	20	20	20	20	15.2	15.2	14.8	14.8	14.2	14.2	13.8	13.8	13.6	13.6	13.6	13.6	13.6	13.4	13.4	13.4	13.4	13.2	13.2
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ОН	Aas09645 Immunorea	ADK46523 INNULOSET Aad48011 BGMV DNAB	Abl75969 Corn tass	Aai61445 Soybean 2	Aai61447 Soybean 2		Aat34008 Primer fo	Abn37518 Human spl	Aaq34156 Downstrea	Aac59405 Human sec	Aac08211 Human sec	Acf56778 Rice endo	Aaq46972 Helper Pr	Aaal5194 PCR prime	Aaa37803 Helicobac	Aba04987 Human tel	Abv76426 Ribosomal	Adb39029 Sample DN	Aaa14518 PCR prime	
ABX81832 AAC80675	AAS09645	ABK46523 AAD48011	ABL75969	AAI 61445	AA161447	ABZ69169	AAT34008	ABN37518	AAQ34156	AAC59405	AAC08211	ACF56778	AAQ46972	AAA15194	AAA37803	ABA04987	ABV76426	ADB39029	AAA14518	
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177	17	33	130	150	150	37	40	9	66	138	182	195	26	27	32	33	41	59	65	
66.0	65.0	65.0	65.0	65.0	65.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	63.0	63.0	63.0	63.0	63.0	63.0	63.0	
13.2	13	13 13	13	13	13	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.6	12.6	12.6	12.6	12.6	12.6	12.6	
25	26	27	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	
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### ALIGNMENTS

20 AAZ10697 standard; DNA; RESULT 1 AAZ10697

BP.

AAZ10697;

(first entry) 23-NOV-1999

p53 activity, UV mimetic, UV-irradiation, UV-induced dermatosis, UV-induced hyperproliferative disease, psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis; photoaging; 

Oligonucleotide sequence that increases p53 activity in a cell.

Synthetic.

skin cancer; ss.

GB2336157-A.

13-OCT-1999.

99GB-00006758. 24-MAR-1999;

98US-00048927 26-MAR-1998;

(UYBO-) UNIV BOSTON.

Eller M; Yaar M, Gilchrest BA,

WPI; 1999-543520/46.

DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases.

Claim 11; Page 30; 44pp; English.

AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are are UV mimetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatcses, reducing photoaging and reducing susceptibility to skin cancer

Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

contain damaged DNA, Also

dd

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apoptosis in epithelial cells that
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                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACD25827 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                            Local Similarity
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YAAR M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACD25827;
                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                            Matches
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88888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Melanin, melanogenic, oligomer, cytostatic, anti-allergic, p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive, DNA repair, proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. psortasis or precancerous conditions); reduce photoacing, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light.
                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention describes inhibition of mammalian epithelial cell
                      100.0%; Score 20; DB 2; Length 20; 100.0%; Pred. No. 1.3;
                                                                                       Indels
                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Melanogenesis associated oligonucleotide #8.
                                                                                   0; Mismatches
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                                                                                                                                                    1 GCATGCATGCATTACGTACG
                                                                                                                                                                                                                                                                                                                                                                     AAS14912 standard; DNA; 20 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-00540843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                   20; Conservative
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                                                      Similarity
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                   Query Match
Best Local S
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                                                                                   Matches
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oligonuclectides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #8, a synthetic peptide that resembles the fragment excissed during excision repair of Thymine dimers and one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting growth of cancer cells and inducing apoptosis in cancer cells, by administering composition having oligonucleotides that share sequence identity with human telomere overhang repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Telomere; ss; probe; cytostatic; human; antipsoriatic; dermatological; apoptosis; cancer; p53; epithelial cell proliferation; DNA damage; lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer; squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1; gp-1100; hyperproliferative disorder; spongiosis; blistering; dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis; actinic keratosis; Bowen's Gisease; basal cell carcinoma; psoriasis; atopic dermatitis; breast cancer; lung cancer; liver cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 20; DB 4; Length 20; 100.0%; Pred. No. 1.3; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
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base= OTHER
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26-MAR-1998; 98US-00048927.
31-MAR-2000; 2000US-00540843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-APR-2002; 2002US-00122630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US010162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "5'
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                   The invention relates to inhibiting growth of cancer cells, which is independent of presence or activity of telomerase in cells, not requiring the presence or activity of p53 normal function in cells, not requiring the presence or activity of p53 normal function in cells, or resulting in 5-phase arrest in cells, and inducing apoptosis in cancer cells, involving administering a composition comprising oligomucleotides which share at least 50% sequence identity with human telomere overhang repeat, (TTAGG)n. The composition may contain 2 of the oligomucleotides (or their contiguous portion) and is used in a method inhibiting proliferation of epithelial cells in a mammal or preventinglyreducing DNA damage in cells of a mammal, where the DNA damage is caused by radiation or DNA-damaging chemicals. The method is useful for inhibiting growth of cancer cells chemically lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer, squamous cell carcinoma), for inducing apoptosis in cancer cells in human, promoting differentiation of malignant cells in a mammal in ammmal in ammmal in ammmal in the context cells in the context of the contex
                                                                                                                                                                                                                                                                                                                                                                                                                                                             enhancing the expression of one or more surface antigens (e.g. MART-1, tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer cells (especially melanoma cells) in a human and for treatment of other hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis in the skin of a mammal, skin cancer in a human with xeroderma pigmentosum, seborrheic keratosis, actinic keratosis, Bowen's disease, or basal cell carcinoma) and for treating or preventing pre-cancerous conditions affecting epithelial cells (such as psoriasis and atopic dermatitis) and also the types of cancers of breast, lung, liver, prostate, pancreatic, ovarian, bladder, uterine, colon, brain, oesophagus, stomach, and thyroid. The present sequence is a melanogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antipsoriatic, dermatological, cancer, apoptosis, skin cancer,
UV irradiation-induced skin, oxidative damage, lymphoma, osteosarcoma,
melanoma, leukaemia, cervical cancer, squamous cell carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ss; human telomere overhang repeat; proliferative disease; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spongiosis; blistering; dyskeratosis; xeroderma pigmentosum; seborrheic keratosis; actinic keratosis; Bowen's disease; basal cell carcinoma; pre-cancerous condition; epithelial cell; psoriasis; atopic dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 20; DB 8; Length 20; 100.0%; Pred. No. 1.3; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonucleotide with homology to telomere pTpT sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     telomere-like oligonucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphorylated"
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/mod base= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCATGCATGCATTACGTACG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-APR-2002; 2002US-00122633
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The invention relates to inhibiting growth of cancer cells (which is independent of the presence or activity of telomerase in cells) not requiring the presence or activity of telomerase in cells) not requiring the presence or activity of ps3 normal function in cells, or requiring the presence or activity of ps3 normal function in cells, or resulting in S-phase arrest in cells, and inducing apoptosis in the cancer cells, comprising administering a composition comprising cliquous clotides which share at least 50% sequence identity with human telomere overhang repeat (TTAGG)n. The method also involves promoting differentiation of malignant cells in a mammal, enhancing the expression of one or more surface antigens indicative of differentiation of cancer cells in a human, by administering the oligonucleotide. The oligonucleotide further administered to enhance repair of uv irradiation-induced danage to the skin in a human, reduce oxidative admands in the composition comprises oligonucleotides such as pagaranced, portace, portaced profit or comprises oligonucleotides such as physiological carrier. Oligonucleotides such as physiological carrier. Oligonucleotides such as physiological carrier. Oligonucleotides such as pracedadGAT praced and proceeding allowed is useful for inhibiting proptosis in cancer cells, pervented cancer, squamous cell carcinoma, melanoma, leukaemia, cervical cancer, squamous cell carcinoma, in a human, promoting differentiation of malignant cells in a mammal and enhancing the expression of one or more surface antigens (e.g. MART-1, tyrosine, TRP-1 or gp-1100) indicative of differentiation of cancer cells, especially melanoma cells, for inhibiting proliferation of epithelial cells in a mammal, where the cells are epithelial cells in enammal, where the cells are epithelial cells. The composition is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                      Inhibiting growth of cancer cells and inducing apoptosis in cancer cells, by administering composition having oligonucleotides that share sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preferably useful for treating a hyperproliferative disorder in human. A composition comprising pGAGTATGAG and pTT, is useful for preventing spongiosis, blistering or dyskeratosis in the skin of a mammal, following exposure to UV light, reducing the occurrence of skin cancer in a human with xeroderma pigmentosum or for enhancing repair of UV irradiationinduced damage to skin in a human, treating melanoma and reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proliferation of keratinocytes in the skin, where the human has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                            identity with human telomere overhang repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             increase pigmentation in melanoma cells
                                                                                                                                                                                                                                                                                                                                                                                 Claim 44; Page 18; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCATGCATGCATTACGTACG 20
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30-MAR-2001; 2001WO-US010162.
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                                                                                                                                                              Gilchrest BA, Eller MS,
                                                  (GILC/) GILCHREST B A. (ELLE/) BLLER M S. (YAAR/) YAAR M.
                                                                                                                                                                                                                   WPI; 2003-512222/48.
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  qq
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ABK91410 standard; DNA; 42

31-MAR-2000; 2000US-00540843

RESULT 5 **ABK91410**  ds; long terminal repeat; LTR; gag; cytostatic; multiple cloning site; envelope protein; retroviral vector; cancer; virally-induced disease;

virucide; gene therapy

WO200260490-A1, 08-AUG-2002.

Synthetic.

31-JAN-2002; 2002WO-US002632 31-JAN-2001; 2001US-0265123P

Gilboa E;

Smith CA,

(UYDU-) UNIV DUKE.

WPI; 2002-619210/66.

Multiple cloning site for retroviral vectors #1.

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The invention relates to a retroviral vector comprising 5' to 3' and in perable linkage, a 5' long terminal repeat (LTR), a splice donor, a packaging sequence, a gag open reading frame (ORF) mutated to reduce translation of gag peptides, a splice acceptor, a start codon in frame infections viral particle comprising transfecting the retroviral vector into a retroviral packaging cell line under conditions to produce the viral particle, and recovering the viral particle, a packaging cell into a retroviral vector, introducing a transcription unit into a cukaryotic cell comprising the retroviral vector, introducing a transcription unit into a cukaryotic cell comprising the retroviral vector, a packaging cell composition comprising the retroviral vector, a packaging cell composition comprising the retroviral vector, a packaging cell composition comprising the retroviral vector, a caukaryotic cell infected by the viral particle and a carrier, diluent, adjuvant or excipient. The vector is useful in expressing a retroviral cell for treating genetic disorders or diseases induced by pathogens such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell for treating genetic disorders or diseases induced by pathogens such as cancer or virally induced disease. The methods are useful for preparing the retroviral vector. The vector provides high titre efficient expression of foreign genes, and safety. The present sequence is a multiple cloning site suitable for inclusion in the vectors of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A new Moloney Murine Leukemia Virus-based retroviral vector, designated as LUV, useful for expressing a retroviral cell for treating genetic disorders, or diseases induced by pathogens such as cancer or virally-induced disease.
                                                                                                                                                                                                                                                                              ds; long terminal repeat; LTR; gag; cytostatic; multiple cloning site; envelope protein; retroviral vector; cancer; virally-induced disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%; Score 15.2; DB 6; Length 42; 85.0%; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 42 BP; 8 A; 13 C; 15 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                Multiple cloning site for retroviral vectors #2.
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                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                    envelope protein; retro
virucide; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gilboa E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-619210/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYDU-) UNIV DUKE.
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                                                                                        05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith CA,
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ABK91410;
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A new Moloney Murine Leukemia Virus-based retroviral vector, designated as LUV, useful for expressing a retroviral cell for treating genetic disorders, or diseases induced by pathogens such as cancer or virally-

Example 1; Page 13; 50pp; English.

induced disease.

The invention relates to a retroviral vector comprising 5' to 3' and in operable linkage, a 5' long terminal repeat (LTR), a splice donor, a packaging sequence, a gag open reading frame (ORF) mutated to reduce translation of gag peptides, a splice acceptor, a start codon in frame translation of gag peptides, a splice acceptor, a start codon in frame confine to but a particle comprising transfecting the retroviral vector into a retroviral packaging cell line under conditions to produce the viral particle, and recovering the viral particle, a packaging cell comprising the retroviral vector, introducing a transcription unit into a cukaryotic cell comprising the retroviral vector, a packaging cell comprising the retroviral vector or the viral particle and a paramaceutical composition comprising the retroviral vector, a call infected by the viral particle, and a carrier, diluent, adjuvant or excipient. The vector is useful in expressing a retroviral cell for treating genetic disorders or diseases induced by pathogens such a cancer or virally induced disease. The methods are useful for preparing the retroviral vector provides high titre, efficient expression of foreign genes, and safety. The present sequence is a multiple cloning site suitable for inclusion in the vectors of the

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                                                                                                                                                                                                                                                                                                                                                                                                               Probe; PCR; terminus; amplify; primer; configuration; ss.
                                                                                                                                                                                                                                                                                           Sequence 42 BP; 6 A; 15 C; 13 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                    Configuration detecting nucleic acid probe #3.
                                                                                                                                                                                                                                                                                                                             1 GCATGCATGCATTACGTACG 20
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                                                                                                                                                                                                                                                                                                                                                                   AAQ95093 standard; DNA; 120 BP.
                                                                                                                                                                                                                                                                                                                                       24 GCGTGCATGCATGCCGTACG
                                                                                                                                                                                                                                                                                                            85.08;
                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                  17; Conservative
                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                              AAQ95093;
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20

1 GCATGCATGCATTACGTACG

Local Similarity 85.0 tes 17; Conservative

Matches

à g

23 degrecardeargedrace 42

BP.

ABK91409 standard; DNA; 42

ABK91409/ RESULT 6

05-NOV-2002 (first entry)

ABK91409;

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Probes (AAQ95091-4) can be used in a method for the detection of a nucleic acid target sequence which has PCR-controlled termini and can be amplified by PCR. The probes can be used to detect configuration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid pUC19; oligonucleotide fragment; DNA detection method; ss.
                                                                                                                                                                                                                                                                                                                          74.0%; Score 14.8; DB 2; Length 120; 88.9%; Pred. No. 6.6e+02; ive 0; Mismatches 2; Indels C
                                                                                                                                                                                                                            Nucleic acid probe - and method for detecting nucleic acid.
                                                                                                                                                                                                                                                                                                        Sequence 120 BP; 30 A; 30 C; 30 G; 30 T; 0 U; 0 Other;
                                             /*tag= a
/note= "PCR primer binding site"
109. .120
                                                                                    /note= "PCR primer binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pCU19 oligonucleotide fragment.
                         Location/Qualifiers
                                                                                                                                                                                                                                                Example 1; Col 4; 6pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                    1 GCATGCATGCATTACGTA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ84038 standard; DNA; 120 BP
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                                                                                                                                                93JP-00133640.
                                                                                                                                                                  93JP-00133640
                                                                                                                                                                                                                                                                                                                                      ilarity 88.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                           /*tag=
                                                                                                                                                                                                        WPI; 1995-069322/10.
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es 16; Conserv
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                                                                                                         JP06343498-A
                                                                                                                                                03-JUN-1993;
                                                                                                                                                                   33-JUN-1993;
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                                                                                                                             20-DEC-1994
                                     primer bind
                                                                  primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
         Synthetic
                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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Method for detecting nucleic acid - using nucleic acid probe and PCR amplification.

WPI; 1995-069323/10.

Example 1; Page 4; 9pp; Japanese.

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression confident nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated prolypeptide or its fragment whose expression is inhibited by the antisense antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a
                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
AAQ84036-Q84040 are oligonucleotide fragments of the plasmid pUC19, they were used in the construction of the plasmid to demonstrate a new method of DNA detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                      Gaps
                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
                                                                                                             Score 14.8; DB 2; Length 120;
Pred. No. 6.6e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
                                                                                Sequence 120 BP; 30 A; 30 C; 30 G; 30 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 claim 14; SEQ ID NO 11843; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Prokaryotic essential gene #5630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                              1 GCATGCATGCATTACGTA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00946993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-MAR-2002; 2002US-0362699P
                                                                                                                   74.0%;
                                                                                                                                                                                                                     24 GCATGCATGCATTATATA
                                                                                                                                                                                                                                                                                                                               ACA23973 standard; DNA; 141
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                        16; Conservative
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-029926/02
                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borrelia cepacia.
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                                                                                                                       Query Match
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Wall D,
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                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
compound's activity, (11) a culture comprising strains in which the gene product is overexpressed or underexpressed, (12) determining the extent to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding region encoding a product active on an essential bacterial target. The method comprises identifying a nucleic acid sequence encoding a gene product that provides a bacteria-inhibiting function when an uncharacterised bacteriophage infects a pathogenic bacterium. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes a method for identifying a bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a bacteriophage coding region for treating bacterial infections comprises identifying a nucleic acid encoding a product that inhibits bacteria when a bacteriophage infects a bacterium.
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage, antimicrobial, genome, identification, antibacterial, bacterial growth inhibition, bacterial infection, ds.
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                                                                                                                                                                                                                                                                                                      71.0%; Score 14.2; DB 7; Length 141; 84.2%; Pred. No. 1.4e+03;
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                                                                                                                                                                                                                                                                     Sequence 141 BP; 28 A; 41 C; 51 G; 21 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage 44AHJD nucleotide sequence 44HJDORF031.
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 278; 456pp; English
                                                                                                                                                                                                                                                                                                                                                                          1 GCATGCATGCATTACGTAC 19
                                                                                                                                                                                                                                                                                                                                                                                                           38 GCCTGCATGCAATACGGAC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
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99US-00407804.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA69048 standard; DNA; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus phage 44AHJD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                     Local Similarity 84.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-412361/35.
P-PSDB; AAB16563.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-2003
27-OCT-2000
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28-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA69048;
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                     Matches
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  compound active on a target of a bacteriophage inhibitor protein in a bacteria is used to treat or prevent a bacterial infection in an animal. AAA68243 to AAB16523 to AAB16524 represent bacteriophage nucleotide and protein sequences which are used in the exemplification of the present invention. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (RAM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunoderection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents one of 5191 Staphylococcus aureus DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyalid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide (s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA;
                                                                                                                                                                                                     0;
                                                                                                                                                         Score 14.2; DB 3; Length 153; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fannon MR,
                                                                                                                                                                                                   3; Indels
                                                                                                                     Sequence 153 BP; 52 A; 21 C; 27 G; 53 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dillon PJ,
                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus contig SEQ ID #1694.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 2035; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barash SC,
                                                                                                                                                                                                                                       1 GCATGCATGCATTACGTAC 19
                                                                                                                                                                                                                                                                              52
                                                                                                                                                                                                                                                                                                                                                                               BP.
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                                                                                                                                                                                                                                                                          70 GCATACCTGCATTACGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97EP-00100117.
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                                                                                                                                                            71.0%;
                                                                                                                                                                            84.2%;
                                                                                                                                                                                                                                                                                                                                                                             AAV76005 standard; DNA; 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-374922/35.
                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.aureus vaccines.
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                                                                                                                                                         Query Match
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AAC21274/c

RESULT 12

Db

Matches

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primers DK15 (AAT29050) and DK16 (AAT29051) were used for the PCR amplification of the ribosome binding site and signal peptide coding regions of the Bacillus stearothermophilus maltogenic alpha-amylase gene in pDNS20. The PCR product was used to construct pPFF1, which also carried a gene (AAT29043) for Oerskovia xanthineolytica beta-1,3-glucanase (AAR97362). Transformation of Bacillus subtilis strain DN1885 or protease-deficient strain ToC46 allowed prodn. of the Oerskovia lytic
                                                                                                                                                                     Beta-1,3-glucanase; Cellulomonas cellulans; Bacillus subtilis; lytic enzyme; beta-glucan degradation; cell wall lysis; pigment; coforant; flavour; yeast extract; protoplast; Oerskovia xanthineolytica; polymerase chain reaction; primer; PCR; alpha-amylase; signal peptide; bacillus stearothermophilus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA construct encoding enzyme with beta-1,3-glucanase activity - useful for modifying or degrading beta-glucan contg. material and in the prepn. of e.g. food colourants, flavourings and yeast extracts.
                                                                                                                                       Maltogenic alpha-amylase signal peptide PCR primer DK16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28 BP; 10 A; 5 C; 8 G; 5 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrer P, Diers I, Hedegaard L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 22; 60pp; English.
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80.0%;
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                   AAT29051 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVO ) NOVO-NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-222000/22
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                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L4-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                WO9612013-A1
                                                                                                   03-OCT-1996
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                                                                                                                                                                                                                                                                                                          Synthetic.
                                                         AAT29051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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AAT29051
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                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
                                                                                                                                                                                                                                                                                                                                                                                                                               Human; 5' BST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                Gaps
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                                    Score 13.8; DB 2; Length 162;
Pred. No. 2.2e+03;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 25349; 71pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic, forensic, gene therapy and chromosome mapping They are used to obtain upstream regulatory sequences and expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 196 BP; 68 A; 35 C; 34 G; 58 T; 0 U; 1 Other;
  Sequence 162 BP; 46 A; 28 C; 33 G; 54 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein 5' EST, SEQ ID NO: 25349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano J;
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                                        ch 69.0%;
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Best Local Similarity
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Score 13.6; DB 2; Length 28; Pred. No. 2.4e+03;
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Matches

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SQ Sequence 76 BP; 18 A; 22 C; 23 G; 13 T; 0 U; 0 Other;

Query Match

Best Local Similarity 80.0%; Pred: No. 2.6e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps
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Search completed: August 11, 2004, 17:56:35 Job time : 292.366 secs BZ411188 OGACTIOTC
CC440642 PUBCYLTE
CC440642 PUBCYLTE
BEB33189 QVJ--CT006
BB737705 BB737705
BH66954 hg92c06.79
BH66954 hg92c06.79
BH66954 hg92c06.79
BH619747 107062C1
CG408774 BB750639
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BG613131 SEP53912
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BG71346 1M0573M21
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BH70277 AM59670.79
BH70273 AM59670.9
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BG7695382 SA9121 CT10804
BG76919 CM1-BT060
BG76919 BK7608931
BG76919 CM1-BT060
BG76919 BK760894

Run on:

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AQ965378 110 bp DNA linear GSS 28-JAN-2000
-LERIB78TR LERG Arabidopsis thaliana genomic clone LERIB78, genomic
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bugnoliophyta, endicotyledons, core eudicots;
rosids, eurosids II, Brassicales, Brassicacae, Arabidopsis.

1 (bases 1 to 110)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polymorphisms
Unpublished (2000)
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
191: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
For addtional information, see http://www.tigr.org/tdb/at/at.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
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AW935636 QV3-DT001
                                                                                           August 11, 2004, 16:50:49 ; Search time 2394.19 Seconds (without alignments) 249.455 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                  27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                                                            of hits satisfying chosen parameters:
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gb_gss2:*
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gb_est4:*

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em_est6!**

em_est6!**

em_est6!**
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Match Length DB
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em_estin:*
                                                                                                                                                     US-09-540-843-8
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em_estov:*
em_estpl:*
                                                                                                                                                                                                                                                                                                                                                                                                                     em_estba:*
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136
142
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Maximum DB seq length: 200
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79.0
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15.8
15.8
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                                                                                                                                                                     score:
                                                                                                                                                                                                                                                                              Total number
                                                                      OM nucleic
                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                  Title:
Perfect :
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No.

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/dev_stage="Adult"
/clone lib="LT0056"
/clone lib="LT0056"
Since="Corgan: leioning, Vector: puc18; Site 1: Smal;
Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142)
1 (bases 1 to 142)
1 bases 1 to 142)
1 (bases 1 to 142)
1 (bases, R., Garvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., O'Hancein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
0 (Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                       AWS81082 136 bp mRNA linear EST 16-MAR-2000 RCI-LT0056-070100-011-all LT0056 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCI&t2=RCI-LT0056-070100-011-a11&t3=2000-01-07&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 136.
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 10; Length 136;
Pred. No. 5.2e+03;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW935636 142 bp mRNA linear
QV3-DT0012-081299-021-£04 DT0012 Homo sapiens CDNA,
                                                                                                                                                                                                                                                                                                 HCGP http://www.ludwig.org.br/ORBSTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                (bases 1 to 136)
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Best Local Similarity 89.5
Matches 17; Conservative
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VERSION
KEYWORDS
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TITLE
JOURNAL
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AW935636/c
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                                                                                                              /mol_type="genomic_DNA"
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/db_xref="teaxon:3702"
/clone="LERIB78"
/clone lib="LERG"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 Kbp before ligation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD725785 127 bp mRNA linear EST 26-JUN-2003 312 Pennisetum glaucum seedlings exposed to salt (500 mM NaCl) Pennisetum glaucum cDNA clone 312, mRNA sequence.
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Paniceae, Pennisetum.
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/dev stage="Two-week-old seedlings"
/clone_lib="Pennisetum glaucum seedlings exposed to salt
(500 mm NaCl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 127)
Mishra,R.N., Markandeya,G., Nair,S., Reddy,A.R., Sopory,S.K. and
Reddy,M.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: Leaf; Vector: Lambda Zap; Site_1: EçoRI; Site_2: Xhol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Reddy MK
Plant Molecular Biology Laboratory
International Centre for Genetic Engineering and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                         Length 110;
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Tel: 91-11-26181242
Fax: 91-11-26162316
Email: redd/@icgeb.res.in.
                                                                                                                                                                                                                                                                                                                         85.0%; Score 17; DB 28; I 100.0%; Pred. No. 1.5e+03;
                                                                                          organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pennisetum glaucum"
/mol_type="mRNA"
/db_xref="taxon:4543"
/clone="312"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                               Location/Qualifiers
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CD725785.1 GI:32276632
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Seq primer: TR
Class: shotgun.
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EST 30-MAY-2000 mRNA sequence.

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CC440642 177 bp DNA linear GSS 20-MAY-2003 PUHGV17TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa448Cl0,
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1 (bases 1 to 177)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4577"
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/clone lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4_TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                   /db_xref="taxon:4577"
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/clone lib="zM_07_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Pred. No. 8.2e+03;
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Pred. No. 5.5e+03;
0; Mismatches 2;
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/strain="B73"
                                                                               /mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ďq
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/organism="Zea mays"
                                                          mays"
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Class: sheared ends.
Location/Qualifiers
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Location/Qualifiers
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Email: whitelaw@tigr.org
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                                                       /organism="Zea
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Other GSSs: PUHGV17TD
Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-DT0012-081Seq primer: puc 18 forward
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1 (bases 1 to 177)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
                                                                                                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                          Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                               Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/organism="Homo sapiens"
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High quality sequence stop: 142.
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Unpublished (2002)
Contact: Cathy Whitelaw
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                                                                                                                                                                    Contact: Simpson A.J.G.
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Class: sheared ends.
                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Fax: +55-11-2707001
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Fax: 301-838-0208
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Tel: 81-45-503-9225

Fax: 81-45-503-9216

Email: genome-resegsc.riken.go.jp,
URL:http://genome-resegsc.riken.go.jp,
URL:http://genome-resegsc.riken.go.jp,
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Computer-based methods for the mouse full-length cDNA
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nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Flease visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC434123 137 bp DNA linear GSS 20-MAY-2003 PUHJB43TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa462H14,
                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okazaki,Y., Osato,K., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Tanaki,T., Tomaru,A., Tayawa,A., Takahashi,F., Takaku-Akahira,S., Muramatsu,M. and Hayashizaki,Y., Watahiki,A., Yasunishi,A., RIKEN Bncyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="spleen"
/dev_stage="6 days neonate"
/clone_lib="RIKEN full-length enriched, 6 days neonate
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/strain="C57BL/6J"
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//organism="Homo sapiens"
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//do_tref="taxon:9606"
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//do_tref="taxon:9606"
//organ:ovary; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 bp mRNA linear EST 15-OCT-2001
BB737705 RIKEN full-length enriched, 6 days neonate spleen Mus
musculus cDNA clone F430015B13 3', mRNA sequence.
BB737705. GI:16136855
EST.
                                                                                                                                                                            Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 199)
Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Goldman,G.H., Carvalho,A.F., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2=QV3-OT0063-120 700-263-h06&t3=2000-07-12&t4=1) seq primer: puc 18 forward High quality sequence start: 7 High quality sequence start: 7 High quality sequence stop: 199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 200)
      QV3-OT0063-120700-263-h06 OT0063 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stringency conditions."
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Mus musculus
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                                                             BE833189.1 GI:10265567
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                                                                                                                           sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, .199
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      DEFINITION
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Gaps

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/mol_type="mRNA"
/db_xref="taxon:73304"
/clone="QHK2H04"
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85.0%;
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                                                                                                                                                                                                                                                                                                                           17; Conservative
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Best Local Similarity
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Best Local Similarity
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Zea mays
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, campanulids, Asterales, Asteraceae, Asteroideae,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="ZMMBTa462H14"
/clone=lb="ZM 0.6 1.0 KB"
/note="Vector: PCK4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA librazy"
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(bases 1 to 155)

Kozik, A., Michelmoze, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; clade; Panicoideae; Andropogoneae; Zea.

(bases 1 to 137)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
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singleton, see http://cgpdb.ucdavis.edu/ for details.
Plate: QHK2 row: H column: 04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 137;
                                                                                                                                                                                                                                                        9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1 - (530) -742-1742
Fax: 1 - (530) -752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 76.0%; Score 15.2; DB 28; Similarity 85.0%; Pred. No. 9.6e+03; 17; Conservative 0; Mismatches 3;
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0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/strain="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                        Tel: 301-838-5843
Fax: 301-838-5843
Email: whitelawætigr.org
Seg primer: TR
Class: sheared ends.
                                                                                                                                              Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUHJB43TD
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                                                                                                                                                                                                            Contact: Cathy Whitelaw
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Matches 17; Conserv
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CF078438
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Thorea—Torgan: inmature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were close, or 8 and 3 kb and were closed in the vector (.X/Y reads in Mi3mpl9, .b/g reads in pUCl9). The same ligation was transformed in either JMIO7 or DH5a. "
                                /clome_lib="QH_K sunflower H.paradoxus" hote="Vector: pRscDNAsfiab; The library was constructed frote="Vector: pRscDNAsfiab; The library was constructed flow four different sources (seedling, root, leaf and flower) of RNA from a single genotype. cDNAs were pooled and directionally cloned into a custom medium-copy vector. Details of library construction can be obtained at http://cgpdb.ucdavis.edu/"
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/clone=hng92co6"
/lab host="An107" or DH5a"
/clone_llb="WGS-ZmaysF" (JM107 adapted_methyl_filtered)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Ratzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Sutarenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenherg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 884
Pax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bg92c06.y8 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays genomic clone hg92c06 5', genomic survey sequence.

BH866954
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/cultivar="B73"
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Location/Qualifiers
1. .165
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Plate: hg92 row: c column: 06
Seq primer: -21M13UnivRev
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/lab_host="E.coli"
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Matches

RESULT 12 BJ250639/c LOCUS

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DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL

COMMENT

FEATURES

ORIGIN

REFERENCE

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/dev stage="adult"
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//dev stage="adult"
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//dev stage="adult"
//dev="lorgan: leaf; Vector: RescueMu (engineered from note="lorgan: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site 1: BamH1; Site 2: BglII;
//devided backbone); Site 1: BamH1; Site 2: BglII;
//devided backbone); Site 1: BamH1; Site 2: BglII;
//devided to allow plasmid rescue from total genomic DNA.
//designed to allow plasmid rescue from total genomic DNA.
//designed to more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid H was grown at Berkeley in 2001. DNA
//devided from leaf punches, double digested using BamH1 and BglII; and ligated to form circular plasmids.
//devided blink ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzeae; Oryza.

1 (bases 1 to 182)
Kim, C.M., Piao, H.L., Park, S.J., Chon, N.S., Je, B.I., Sun, B.,
Fark, S.H., Park, J.Y., Lee, E.J., Kim, M.J., Lee, J.J., Nam, M.H.,
Eun, M.Y. and Han, C.D.
Rapid, large-scale generation of Ds transposant lines and analysis
Of Ds loci in rice
                                             Email: walbot@stanford.edu
possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1007062 column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ds467 Ds insertion lines Oryza sativa (japonica cultivar-group)

    182
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 171;
                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 1e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Chang-deok Han
Division of Applied Life Science, PMBBRC
Gyeongsang National University
Gazwa-dong 900, Jinju 660-701, South Korea
Tal: +82 55 751 6029
Fax: +82 55 759 9363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 bp
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                                                                                                                                                                                                                         organism="Zea mays"
                                                                                                                                            Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       tissue_type="leaf"
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85.0%;
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rel: 650 723 2227
                         Fax: 650 725 8221
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Best Local Similarity
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CG408774/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Spoideae, Triticeae, Triticum.

1 (bases 1 to 16)
Ogihara, Y. and Murai, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryóta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 171)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/oulfivar="Chinese Spring"
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/tissue_type="spike at flowering date"
/tissue_type="spike at flowering date"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh_f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
  Gaps
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BJ250639
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Contact: Tadata Shin-i
Contact: Tadata Shin-i
Conter: Tracta Sesource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.0%; Score 15.2; DB 12;
85.0%; Pred. No. 1e+04;
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  0; Mismatches
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Stanford University
                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                         141 GCATGCACGCTGTACGTACG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 GCATGCATGTATTGCGTGCG 112
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                                                   1 GCATGCATGCATTACGTACG 20
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  17; Conservative
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DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

RESULT 13 BH619747 LOCUS

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0

Gaps

0;

GSS 03-SEP-2003

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/note="Vector: pSPORTI; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into pSPORTI. Derived from roots of 3 week old drought stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating
                                                                                                          ó;
                                                                                                                                                                                                                                                EST 23-JUL-2002
                                                                                                                                                                                                                                                         EBroo8 SQ004 C17 R root, 3 Week, drought-stressed, ov Optic, EBroo8 Hordeum vulgare Subsp. vulgare cDNA clone EBroo8_SQ004_C17 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="root, 3 week, drought-stressed, cv Optic,
BBro08"
                                                                                                            Gaps
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                                                                          Length 182;
                                                                                                                                                                                                                                              linear
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/organism="Hordeum vulgare subsp. vulgare"
                                                                                                          Indels
                                                                            29;
/cultivar="Dongjin"
/db_xref="taxon:39947"
/clone_lib="Ds insertion lines"
                                                                                                                                                                                                                                              mRNA
                                                                         Score 15.2; DB 2
Pred. No. 1e+04;
0; Mismatches
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cultivar="Optic"
sub_species="vulgare"
db_xref="teaxon:112509"
clone="EBro08 SQ004_C17"
flasue_type="root"
dev_stage="3 week"
lab_host="DH108"
                                                                                                                                                                                                                                              183 bp
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                                                                                                                                                          118 GCATGCATGCATGACACACG 99
                                                                                                                                       1 GCATGCATGCATTACGTACG 20
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BM370416.1 GI:18113806
                                                                       ch 76.0%;
1 Similarity 85.0%;
17; Conservative
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Best Local Similarity 85.0
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COMMENT
                                                                                                                                                                                                              RESULT 15
BM370416
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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Search completed: August 11, 2004, 18:58:49

116 GCATTCATGTACTACGTACG 135

1 GCATGCATGCATTACGTACG 20

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Job time : 2400.86 secs

(0108N) YUD18 860d S141

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August 11, 2004, 17:57:26 ; Search time 60 Seconds (without alignments) 184.984 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                              OM nucleic - nucleic search, using
                                                                                                                                                    Run on:
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US-09-540-843-8 Title: Perfect score:

682709 segs, 277475446 residues 1 gcatgcatgcattacgtacg 20 IDENTITY NUC Gapop 10.0 Gapop 10.0 Scoring table: Sequence: Searched:

979464 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

/cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
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/cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\* Issued Patents NA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

1,000		<b>*</b>				
No.	Sco	Query Match	Query Match Length	DB	ID	Description
1	13.8	69.0	162	4	US-08-956-171E-1694	Semence 1694. Ap
2	13.6	68.0	28	Н	-982-712-34	34 Ar
с 3	1	68.0		r*f	-07-982-712-3	i in
C 4	13.4	67.0	28	٦	-5	10,
5	13.4	67.0	42	Н	US-08-301-872A-6	6.7
9	13.4	67.0	42	7	-08-4	Segmence 6, Appli
c 7	13.4	67.0	70	Н	- 1	7
80	13.4	67.0	7.0	Н	US-08-301-872A-8	8
0	1	•	70	N	US-08-443-372A-7	7
10	~1	67.0	70	7	US-08-443-372A-8	8
11	13.2	0.99	33	4	US-09-535-851A-6	9
c 12	13.2	0.99	177	4	US-09-313-294A-292	292
13	12.6		26	Н	US-07-720-586-7	-
c 14	12.	63.0	65	æ	US-09-415-522-24	24
c 15	М	63.0	108	4	US-08-956-171E-4834	483
c 16	7	63.0	129	4	US-08-956-171E-4790	4790.
17	12.6	63.0	178	4	US-09-313-294A-26	26. At
18	٦	S	38	C)	US-09-097-759-6	. 9
19	-	62.0	e	m	US-09-065-104-24	24
c 20	7	N	Ŋ	~	US-08-816-155B-23	N
	1	N	59	m	US-08-815-809-8	8
CI	7	62.0	59	m	US-09-079-587-23	23
7	1	2	138	Н	US-08-600-234-5	Sequence 5, Appli
	7	N	138	Н	US-08-386-921-5	'n
c 25	12.4	5	141	Н	US-08-386-921-13	13,
c 26	7	62.0	144	Н	US-08-386-921-11	Н
c 27	12.4	62.0	147	Н	US-08-386-921-9	o

Sequence 2, Appli Sequence 10, Appli Sequence 11, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 43, Appli Sequence 15, Appli Sequence 15, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli	Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl
US-08-600-234-2 US-08-386-921-2 US-08-386-921-10 US-08-386-921-10 US-08-294-3128-21 US-08-468-0248-21 US-08-465-679-21 US-08-4187-7570-19 US-08-110-143C-19 US-09-510-143C-19 US-09-510-143C-15 US-09-360-376-4 US-09-360-376-4 US-09-453-623-18	US-08-961-810-31 US-08-352-902D-31 US-09-265-503B-31
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0 0 0 0 0 0 0 0 0	υυυ

### ALIGNMENTS

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Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5.256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-0ct-1997
CLASSIFICATION AURINOMD.
PRIOR APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTOREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; SEQUENCE DESCRIPTION: SEQ ID NO: 1694: US-08-956-171E-1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFRENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1124
TELEFAX: (301) 309-8439
                                               ; Sequence 1694, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1694:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Maryland
COUNTRY: USA
RESULT 1
US-08-956-171E-1694
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Length 58;
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Sequence 10, Application US/08053564

Sequence 10, Application US/08053564

Patent No. 5418151

APPLICANT: MORI, MASASHI

APPLICANT: OKUNO, TRISTORO

APPLICANT: FURUSAWA IWAO

ITILE OF INVENTION: EXCGENOUS GENE OR ITS PRODUCT

TITLE OF INVENTION: IN PLANT CELLS NO.2

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match

68.0%; Score 13.6; DB 1;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 4;
                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.50 inch, 144 mb
COMPUTER: IBM Compatible
OPREATING SYSTEM: MS-1005
SOGTWARE: Wordperfect 5.1
CURRENT APPLICATION UDMER:
APPLICATION UNDMER: US/07/982,712
FILING DATE: 19921127
CLASSIFICATION: 800
PRIOR APPLICATION BATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.25 CURRENT APPLICATION DATA:
                                                                 Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sughrue, Mion, Zinn, Macpeak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
                                          Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
US-07-982-712-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REPERENCE/DOCKET NUMBER: TELECOMMUNICATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 bases
                                          ADDRESSEE: Wenderoth, STREET: 805 Fifteenth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QUENCE CARACTER 58 bases
IYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                           ZIP: Z0005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                         CORRESPONDENCE ADDRESS:
NUMBER OF SEQUENCES:
                                                                                            Washington
                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
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ADDRESSEE:
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                                                                                                                                                                                                                                           | Sequence 34, Application US/07982712 | Sequence 34, Application US/07982712 | Patent No. 5446391 | Sexemence 34, Application US/07982712 | Sexemence 34, Application Sequence 34, Applicant Hideya FUJIMOTO, Kimiko ITOH APPLICANT: Hideya FUJIMOTO, and Ko SHIMAMOTO TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS: ADDRESSE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 35, Application US/07982712
Sequence 35, Application US/07982712
Patent No. 5436391
GENERAL INFORMATION:
APPLICANT: Hideya FUJIMOTO, Kimiko ITOH
APPLICANT: Mikihiro YAMAMOTO, and Ko SHIMAMOTO
APPLICANT: Mikihiro YAMAMOTO, and Ko SHIMAMOTO
TITLE OF INVENTION: Insecticidal Protein-encoding Gene, Gramineous
TITLE OF INVENTION: Plants Transformed with the Gene, and Production Thereof
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69.0%; Score 13.8; DB 4; Length 162; 88.2%; Pred. No. 3.2e+02; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 144 mb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 GCATGCATGAATTCCCTAGG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                    4 TGCATGCATTACGTACG 20
                                                                                                                                                 50 TACATGCAATACGTACG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/
FILING DATE: 19921127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 58 bases
       Query Match
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Score 13.4; DB 1; Length 42; Pred. No. 4.5e+02;
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Patent No. 5869339
GENERAL INFORMATION
PAPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32,227
PD. TKT90-01A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-08-301-872A-7/c
; Sequence 7, Application US/08301872A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Granahan, Patricia
REGIESTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
             MOLECULE TYPE: DNA (genomic)
                                                                           67.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.0%;
                                                                                                                                                               5 GCATGCATTACGTAC 19
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LENGTH: 42 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 93.3'
                                                                                               Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
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                 ;
US-08-301-872A-6
                                                                                                                                                                                                                                                                  RESULT 6
US-08-443-372A-6
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STATE:
                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
CORRESPONDENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301,872A
FILING DATE: 06-SEP-1994
CLASSIFICATION NUMBER: US/08/301,872A
FILING DATE: 06-SEP-1994
APPLICATION NUMBER: US/739,861
FILING DATE: 02-AUG-1991
PRIOR APPLICATION NUMBER: US 07/739,861
FILING DATE: 02-AUG-1991
APPLICATION NUMBER: US 07/552,183
FILING DATE: 13-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT90-01A2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Other nucleic acid DESCRIPTION: synthesized oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
APPLICATION NUMBER: US/08/053,564
FILING DATE: 28-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 28-APR-1992
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08301872A Patent No. 5580734 GENERAL INFORMATION:
                                                                                                                                                                                                                             10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CATGCATGCATTACG 16
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Best Local Similarity 93.33
France 14; Conservative
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                                                                                                                                                                                                  TELEX: 649113
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 42 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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US-08-301-872A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: I
STATE:
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ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Elb PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PEL PEL PC COMPUTER:
COMPUTER: PACHION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,372A
FILING DATE: 17-MAY-1995
CLASSIFICATION ADATA:
APPLICATION NUMBER: US 08/301,872
FILING DATE: 06-SEP-1994
APPLICATION NUMBER: US 07/739,861
FILING DATE: 07-AUG-1991
RILING DATE: 03-AUG-1991
RILING DATE: 13-JUL-1990
ATTONEY/AGENT INPOMENTION
NUMBER: US 07/552,183
FILING DATE: 13-JUL-1990
ATTONEY/AGENT INPOMENTION
NUMBER: DATAILING DATE: DATAILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13.4; DB 2;
Pred. No. 4.5e+02;
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PatentIn Release #1.0, Version #1.30
                                                                              FILING DATE: 06-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/739,861
FILING DATE: 02-AUG-1991
PRIOR APPLICATION DATA: 07/552,183
FILING DATE: 13-UU-1990
ATTORNEY, AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT90-01A2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION INFORMATION I
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                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301,872A
FILING DATE: 06-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP. 02173
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CATGCATTACGTACG 20
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Best Local Similarity 93...
Best Local 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Lexington STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Treco, Douglas A. APPLICANT: Treco, Douglas A. TITLE OF INVENTION: Library Screening Method NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Lexington
                                                       APPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: C-LOUS/NS-LUOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301,872A
FILING DATE: 06-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/739,861
FILING DATE: 02-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/552,183
FILING DATE: 13-ULL-1990
ATORNEY/AGENT INFORMATION:
NAME: Granaban, Patricia
REGISTRATION NUMBER: 32,227
REBERNEK/DCOKET NUMBER: 32,227
REBERNEK/DCOKET NUMBER: TKT90-01A2
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKT90-01A2
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COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 CATGCATTACGTACG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: double
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   ; Patent No. 5580734
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                   CITY: Lexing
STATE: MA
COUNTRY: USI
ZIP: 02173
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Gaps
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Length 70;
                                                      Indels
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Patent No. 5869239
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
NUMBER OF SEQUENCES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FLING DATE:

APPLICATION NUMBER:

CLASSIFICATION:

APPLICATION NUMBER:

CLASSIFICATION NUMBER:

BRICK APPLICATION NUMBER:

APPLICATION NUMBER:

CLASSIFICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

ATTORNEY/AGENT INFORMATION:
Score 13.4; DB 1;
Pred. No. 4.7e+02;
0; Mismatches 1;
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Pred. No. 4.7e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08443372A
Patent No. 5865239
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Miller, Allan M.
TITLE OF INVENTION: Library Screening Method
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIN APPLICATION DATA:
APPLICATION NUMBER: US/08/443,372A
FILING DATE: 17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 32,227
RELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/301,872
FILING DATE: 06-SEP-1994
APPLICATION NUMBER: US 07/739,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/739,861
FILING DATE: 02-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/552,183
FILING DATE: 13-UUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
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Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                            6 CATGCATTACGTACG 20
                                                                                                                                                                                                                                                                                                                                                                               54 CATGCATTACGTAGG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617-861-6240
617-861-9540
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 93.33
Matches 14; Conservative
                                                                                                          70 base pairs
                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-MAY-:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                          linear
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                                                                                                                                                                      TOPOLOGY:
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Gaps

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Sequence 6, Application US/09535851A

Parent No. 6528636

GENERAL INFORMATION:
APPLICANT: Battelle Memorial Institute
TITLE OF INVENTION: A Promoter Sequence of 3-Phosphoglycerate Kinase Gene 2 of Lactic
TITLE OF INVENTION: A Producing Fungus Rhizopus Oryzae and a Method of Expressing a Ger
TITLE OF INVENTION: in Fungal Species
TITLE OF INVENTION: in Fungal Species
FILE REFERENCE: E-1891B
CURRENT APPLICATION NUMBER: US/09/535,851A
CURRENT FILING DATE: 2000-03-27
NUMBER OF SEQ 1D NOS: 9
SOFTWARE PATENT OF NOS: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman Bradley K.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REPERBACE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
NUMBER OF SEQ ID NOS: 7600
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CTHER INFORMATION: Incyte ID No. 6476212 700548929H1

NAME/KEY: unsure

LOCATION: 2, 6, 75-93

COTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.0%; Score 13.2; DB 4;
83.3%; Pred. No. 6.4e+02;
live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: oligonucleotide primer US-09-535-851A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCATGCATGCATTACGTA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GCATGCATGTATTTCATA 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
                                        17 cardcarraccraes 31
  6 CATGCATTACGTACG
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER PER SOFTWARE: PER SEQ ID NO 292
                                                                                                                                   US-09-535-851A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 6
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US-08-956-171E-4834/c

Sequence 4834 Application US/08956171E

Sequence 4834 Application US/08956171E

Patent No. 6593114

GENERAL INFORMATION:
GENERAL INFORMATION:
GILH. Charles Kunsch
Gil H. Choi

Patentick S. Dillon
Craig A. Rosen

Steven C. Barash
Michael R. Pannon

TITLE OF INFORMATION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-06-1997

CLASSIFCATION: CURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/09,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
ATORNEY/AGENT INFORMATION:
NAME: MARK J. HYMMEN
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 46,789
                                                          FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence:Primer
US-09-415-522-24
                                                                                                                                                                                         Length 65;
                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                      Score 12.6; DB 3;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 4834:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 108 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CATGCATGCATTACGTACG 20
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            1 GCATGCATGCATTACGTAC 19
                                                                                                                                                                                                                                                                                                                                                                                          57 derrecardecrirearae 39
                                                                                                                                                                                         63.0%;
78.9%;
                              ORGANISM: Artificial Sequence
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Best Local Similarity 78.9°
Matches 15; Conservative
                                                                                                                                                                                             Query Match
Best Local Similarity 78.9°
Matches 15; Conservative
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TYPE: DNA
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Sequence 24, Application US/09415522A
Patent No. 6291660
GENERAL INFORMATION:
APPLICANT: Gaffney, Thomas
APPLICANT: Gaffney, Thomas
APPLICANT: Philippsen, Peter
TITLE OF INVENTION: No. 6291660el Fungal Genes Required For No. 6291660mal Growth And
TITLE OF INVENTION: Development
FILE REFERENCE: CGC2040
CURRENT APPLICATION NUMBER: US/09/415,522A
CURRENT FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5." Diskette, 1.44 Mb storage

MEDIUM TYPE: 3.5." Diskette, 1.44 Mb storage

COMPUTER: 18M PS/2 Model 50Z or 55SX

OPERATING SYSTEM: 1BM P.C. DOS (Version 3.30)

SOFTWARE: 18910628

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/720,586

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER:

PILING DATE:

APPLICATION UNMBER:

PILING DATE:

REGISTRATION NUMBER:

REGISTRATION NUMBER:
                                                                                                                                                       APPLICANT: Curt Milliman
APPLICANT: Philip W. Hammond
APPLICANT: Philip W. Hammond
TITLE OF INVENTION: UNCLEIC ACIDS PROBES
TITLE OF INVENTION: TO STREPTOCOCCUS PYOGENES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
                                                                 ; Sequence 7, Application US/07720586; Patent No. 5232831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 193, TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600 TELEFAX: (213) 955-0440 TELEX: 67-3510 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CATGCATGCATTACGTACG 20
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roporogy: linear
                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-09-415-522-24/C
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SEQ ID NO 24
LENGTH: 65
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Search completed: August 11, 2004, 19:33:24 Job time : 61 secs

(otasu) Andla egod sint

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Sequence 11844, A Sequence 32, Appl Sequence 32, Appl Sequence 32687, A Sequence 1694, Ap Sequence 1694, Ap Sequence 1569, Ap Sequence 59127, A Sequence 46744, A Sequence 18933, A
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Sequence 8, Appli
                                                                                                                                                              August 11, 2004, 19:00:04; Search time 288.387 Seconds (without alignments) 340.279 Million cell updates/sec
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| cgn2 6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2 6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
3: /cgn2 6/ptodata/2/pubpna/USO6_DEW PUB.seq:*
4: /cgn2 6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2 6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
6: /cgn2 6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2 6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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9: /cgn2 6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2 6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
112: /cgn2 6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
12: /cgn2 6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2 6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
14: /cgn2 6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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16: /cgn2 6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*
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18: /cgn2 6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*
19: /cgn2 6/ptodata/2/pubpna/USOOB_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-122-633-8

10-10-28-122A-11843

2 US-09-727-892-32

7 US-10-437-963-71654

7 US-10-437-963-71654

7 US-08-781-986A-1694

3 US-10-424-599-76449

3 US-10-424-599-1569

3 US-10-424-599-76527

7 US-10-437-963-46444

3 US-10-424-599-76527

7 US-10-437-963-46444

3 US-10-437-963-46444
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                                                                                                               OM nucleic - nucleic search, using sw model
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY NUC
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Maximum DB seq length: 200
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Sequence 18933, A Sequence 87658, A	656, App e 129131,	431 516	e 65	5712,	6262,		Sequence 66570, A	95	854	equence 855,	494	5343	9 76,		2073		Sequence 10266, A		97,	59525,	Sequence 62748, A	4801	169,	4	
6 US-10-242-535A-18933 7 US-10-437-963-B7658 7 US-10-031-33-16967	US-10-424-559 US-10-424-599-1291	US-US-969-373-431 US-09-969-373-516	3 US-10-424-599-65688 7 US-10-437-963-96687	US-10-260-238-571	US-10-085-783A	US-10-242-535A-62	US-10-424-599-6 TIS-10-424-599-3	-035-95	US-09-969-373-854	US-09-969-373-855	US-09-969-373-494	US-09-294-093B-5343	US-09-754-853A-7	US-09-754-853A-78	US-09-923-876-2073	3-876	8-97	US-09-969-373-16	US-10-437-	US-10-424-599-59525		US-10-424-599-4	US-09-969-373-169	US-10-147-368-4	
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### ALIGNMENTS

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Sequence 8, Application US/10122630

Sequence 8, Application US/10122630

Sequence 8, Application VS 020030032610A1

Sequence 8, Application No US20030032610A1

APPLICANT: Gllchrest, Barbara A. APPLICANT: Gllchrest, Barbara A. APPLICANT: Eller Mark S. APPLICANT: Year, Mina APPLICANT: Year, Mina C. TITLE OF INVENTION: Oligonuclectides

TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonuclectides

FILE REFERENCE: 0054-1088-018

CURRENT APPLICATION NUMBER: US 08/467,012

PRIOR APPLICATION NUMBER: US 08/467,012

PRIOR APPLICATION NUMBER: DS 06-66

PRIOR APPLICATION NUMBER: DS 06-66

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-36

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: PCT/US01/10162

PRIOR APPLICATION: Synthetic DNA Fragment
US-10-122-630-8

QUETY MATCH

Best Local Similarity 100.0%; PCT-US01/1063

Best Local Similarity 0.0 17 PER PCT/US01/1063

PRIOR PCT/US01/1062

PRIOR PCT/US01/1063

PURCANISM: PCT/US01/1063

PURCANISM:
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Best Local Similarity
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US-09-727-892-32/c
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
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100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                               APPLICANT: Glichrest, Barbara A.
APPLICANT: Glichrest, Mark S.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REPERENCE: 0054.1089-019
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US/10/12,633
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR FILING DATE: 2001-03-31
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic DNA Fragment US-10-122-633-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-282-122A-11843/c
Sequence 11843, Application US/10282122A
Publication No. US20040029129A1
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APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/230,335
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                                                                                                                                                                 ; Sequence 8, Application US/10122633; Publication No. US20030032611A1; GENERAL INFORMATION:
GCATGCATGCATTACGTACG 20
                                            gcargcargcarracgracg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamancto, Robert
APPLICANT: Yamancto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                         RESULT 2
US-10-122-633-8
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APPLICANT:
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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APPLICANT: Phagetech, Inc.
APPLICANT: PELETIER, Jerry
APPLICANT: GROS, Philippe
APPLICANT: GROS, Philippe
APPLICANT: GROS, Philippe
TITLE OF INVENTION: DNA SEQUENCES FROM STAPHYLOCOCCUS AUREUS BACTERIOPHAGE 44 AHUD
TITLE OF INVENTION: THAT ENCODE ANTI-MICROBIAL POLYPEPTIDES
FILE REFERENCE: 073406-0309/727,892
CURRENT APPLICATION NUMBER: US/09/727,892
CURRENT FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 159
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 32
LENGTH: 153
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PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,931
PRIOR PLING DATE: 2010-10-29
PRIOR FILING DATE: 2010-10-20
PRIOR FILING DATE: 2010-10-20
PRIOR FILING DATE: 2010-10-20
PRIOR FILING DATE: 2010-10-216
PROBABLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2010-10-216
PROBABLICATION NUMBER: 00/269,308
PROBABLICATION NUMBER: 00/269,308
PROBABLIS SEQ ID NOS: 78614
SOFTWARE PARENTIN VERSION 3.1
SEQ ID NO 11843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.0%; Score 14.2; DB 13; Best Local Similarity 84.2%; Pred. No. 2.7e+03; Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 71654, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 32, Application US/09727892; Publication No. US20040091856A1; GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihuua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Burkholderia cepacia
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APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5.256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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    MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
COMPATING SYSTEM: MSDOS version 6.2
SOFTWARE: AGCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 13.8; DB 8;
Pred. No. 4.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 60/009,861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
                                                                                                                                                                                                                                           ATTOREY/AGENT 111.

NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REGISTRATION NUMBER: PB246PP
TELECOMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
; TELEPHONE: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 1694:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: duble
; TYPE: nucleic acid
; TYPE: nucleic acid
; TYPE: nucleic acid
                                                                                                                   APPLICATION NUMBER: US/08/781,986A FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1694, Application US/10329624 Publication No. US20040043037A1 GENERAL INFORMATION:
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Best Local Similarity 88.2%;
Matches 15; Conservative
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COMPUTER READABLE FORM:
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                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
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US-10-329-624-1694
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| Sequence 32687, Application US/10437963
| Sequence 32687, Application US/10437963
| Publication No: US20040123343A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Cao, Yougwei |
| APPLICANT: Cao, Yougwei |
| APPLICANT: Barbazuk, Brad |
| APPLICANT: Barbazuk, Brad |
| APPLICANT: Li, Ping |
| TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| TITLE REFERENCE: 38-21 (53221) B |
| CURRENT APPLICATION NUMBER: US/10/437,963 |
| CURRENT FILING DATE: 2003-05-14 |
| SEQ ID NO 32687 |
| LINGTH: 191
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Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
ATTLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                         Length 175;
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Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                         Score 14.2; DB 17;
Pred. No. 2.8e+03;
                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT MRT4530 72107C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_36871C.1
US-10-437-963-32687
                                                                                                                                                                                                                                                                                                                      0; Mismatches
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FILE REFERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
SEQ ID NO SEQ ID NOS: 204966
LENGTH: 175
                                                                                                                                                                                                                                                                                                                                                                  2 CATGCATGCATTACGTACG 20
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Best Local Similarity 84.2%;
Matches 16; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                     TYPE: DNA ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                            US-10-437-963-71654
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Length 177; Indels

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Sequence 76527, Application US/10424599
; Sequence 76527, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cavalic David K
; APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 76527
LENGHH: 187
                                                                                                                                                                                                                                                                                                                                      Squence 59127, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-64-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS 285681
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88.2%; Pred. No. 4.3e+03;
live 0; Mismatches 2;
              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_101416C.1
US-10-424-599-1569
                                                                   Query Match 69.0%; Score 13.8; DB 13;
Best Local Similarity 88.2%; Pred. No. 4.3e+03;
Constitute 0: Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_40115C.1
US-10-424-599-76527
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OTHER INFORMATION: unsure at all n locations
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                                                                                                                                                                                          3 ATGCATGCATTACGTAC 19
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
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US-10-424-599-76527
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With;
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement;
FILE REFRENCE: 38-21(5223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: About Shud
APPLICANT: About Shud
APPLICANT: About Shud
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 76449
LENGTH: 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_40045C.1
US-10-424-599-76449
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
                                                                                                                                                                                     ;
TOPOLOGY: linear
sEQUENCE DESCRIPTION: SEQ ID NO: 1694:
US-10-329-624-1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 76449, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                              TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 16943
SEQUENCE CHARACTERISTICS:
                                                                                                                                           LENGTH: 162 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 88.2%
Matches 15; Conservative
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TYPE: DNA
ORGANISM: Glycine max
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US-10-424-599-1569
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Gaps

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**Sequence 18933, Application US/10242535A; Bublication No. US20040013663A1

**Sequence 18933, Application No. US20040013663A1

**Sequence 18933, Application No. US20040013663A1

**Sequence 18933, Application No. US20040013663A1

**APPLICANT: ChondroGene Inc.

**APPLICANT: Compositions and Methods Relating to Osteoarthritis

**FILE REFERENCE: 4231/2005

**CURRENT APPLICATION NUMBER: US 10/085,783

**PRIOR APPLICATION NUMBER: US 60/305,340

**PRIOR FILING DATE: 2001-07-18

**PRIOR FILING DATE: 2001-07-18

**PRIOR APPLICATION NUMBER: US 60/275,017

**PRIOR APPLICATION NUMBER: US 60/271,955

**PRIOR APPLICATION NUMBER: US 60/271,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                    1 GCATGCATGCATTACGTACG 20
                                                                          65 GCTTTCATGCATTACCTAAG 46
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Matches 16; Conserv
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US-10-242-535A-18933/c
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ORGANISM: Human
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 46744
LENGTH: 112
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ITILE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT FILING DATE: 2002-02-28

PRIOR PAPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SOPTWARE: Patentin version 3.2

LENGTH: 165
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68.0%; Score 13.6; DB 13; Length 165;
Best Local Similarity 80.0%; Pred. No. 5.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0
  88.2%; Pred. No. 4.4e+03;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                               Sequence 46744, Application US/10437963
PUblication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
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US-10-085-783A-18933/c
; Sequence 18933, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCATGCATGCATTACGTACG 20
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                                                                                                                                90 TGCATGCATTGCCTACG 106
                                                                                         4 TGCATGCATTACGTACG 20
                                15; Conservative
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ORGANISM: Oryza sativa
Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 16; Conserv
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US-10-437-963-46744
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APPLICANT:
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 11, 2004, 17:38:14; Search time 317.419 Seconds (without alignments) 682.741 Million cell updates/sec Run on:

US-09-540-843-6 5 1 catac 5 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

3470272 segs, 21671516995 residues Searched:

2199298 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200 Minimum DB s Maximum DB s

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

GenEmb1:\* Database

gb ba: \*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Res	Result		Query					
i	No.	Score	Match	Length	DB	ID	Descripti	cion
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ALIGNMENTS

Sequence 4 from Patent W00174342. AX268756 AX268756.1 GI:16541828 RESULT 1
AX268756/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

PAT 29-OCT-2001

linear

DNA

synthetic construct synthetic construct artificial sequences.

REFERENCE AUTHORS TITLE JOURNAL

dilchrest,B.A., Yaar,M. and Eller,M.
Use of locally applied dna fragments
Patent: WO 0174342-A 4 11-OCT-2001;
TRUSTEES OF BOSTON UNIVERSITY (US)

FEATURES

ORIGIN

RESULT 2 AX268758

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VERSION

FEATURES

ORIGIN

TITLE

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Motivor, RS., Hackett, P.B. and Aguilar-Cordova, B.

Vector-mediated delivery of integrating transposon sequences
Patent: WO 0068399-A 6 16-NOV-2000;

REGENTS OF THE UNIVERSITY OF MINNESOTA (US); BAYLOR COLLEGE OF
MEDICINE (US); MCIVOr, R. Scott (US); Hackett, Perry B. (US);
Aguilar-Cordova, Estuardo (US)
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                                                                                                                                                          linear
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                   Indels
    Pred. No. 6.2e+09;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 100.0%; Score 5; DB 6; Lu Similarity 100.0%; Pred. No. 6.2e+09; 5; Conservative 0; Mismatches 0;
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/mol_type="genomic DNA"
/do_xref="taxon:32630"
/nofc="Direct Repeat Sequence"
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/mol type="genemic DNA"
| Mol type="genemic DNA"
| Abore="synthetic DNA Fragment"
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100.0%; Pred. ..-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX047565 8 bp. Sequence 6 from Patent WO0068399. AX047565
                                                                                                                                                     7 bp
Sequence 7 from Patent W00174342.
AXZ68759
AXZ68759.1 GI:16541831
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/organism="synthetic construct"
/nol_type="genomic DNA"
/db xref="taxon:32630"
/noTe="Synthetic DNA Fragment"
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/mol_type="genomic DNA"
/do_xref="taxon:32630"
/nofe="Synthetic DNA Fragment"
                         /note="Synthetic DNA Fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Gilchrest, B.A., Yaar, M. and Eller, M. Use of locally applied dna fragments Patent: WO 0174342-A 6 11-OCT-2001; TRUSTEES OF BOSTON UNIVERSITY (US)
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Sequence 6 from Patent WO0174342.
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8 bp DNA linear PAT 17-JUL-2003 DNA linear PAT 17-JUL-2003 Into DNA of a cell.
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Strandedness: Single;
                            Artificial sequences.

1 (bases 1 to 8)
Hackett, P.B., Clark, K.J., Dapie, A.J., Ekar, S.C., Larjespayda, D.A.,
Ibycus, Z. and Issufark, T.
DNA-based transposon system for the introduction of nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 8)
Hackett, P.B., Ivics, Z., Izsvak, Z. and Caldovic, L.
DNA-based transposon system for the introduction of nucleic acid
into DNA of a cell
batent: JP 2002511741-A 10 16-APR-2002;
PREGNIS OF THE UNIV OF MINNESOTA
PD 16-APR-2002
PP 11-ARR-1998 JP 1998539720
                                                                                                                                                        into DNA of a cell
Patent: JP 2001523450-A 10 27-NOV-2001;
Predent: JP 2001523450-A 10 27-NOV-2001;
Predent: JP 2001523450-A 10 27-NOV-2001;
Production of much product production of much production of mu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2002511741-A/10.
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                                                           PAT 30-APR-2001
                                                                                                                                                                     synthetic construct
synthetic construct
artificial sequences.

1 (bases 1 to 8)
KriseyA.M., Schetter,C. and Vollmer,J.C.
Immunostimulatory nucleic acids
Patent: WO 0122972-A 1138 05-APR-2001;
UNIVERSITY OF IOWA RESERARCH FOUNDATION (US); Coley Pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT 11-MAY-2001
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DNA-based transposon system for the introduction of nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 8)
Messiaen, L. and Callens, T.
Improved mutation analysis of the nfl gene
Patent: WO 0129251-A 224 26-APR-2001;
UNIVERSITEIT GENT (BE)
Location/Qualifiers
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                                              8 bp DN Sequence 1138 from Patent W00122972. AXI04946 AXI04946.1 GI:13921143
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Sequence 224 from Patent WO0129251.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 5;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/db_xref="taxon:32630"
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BD085298.1 GI:22630908
JP 2001523450-A/10.
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Similarity 100.0%;
5; Conservative 0
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Position dependent recognition of gnn nucleotide triplets by zinc
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ilarity 100.0%; Pred. No. 4.8e+09;
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Patent: WO 0242459-A 2256 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Patent: WO 0242459-A 2220 30-MAY-2002;
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Sequence 2220 from Patent WO0242459.
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Sequence 43 from Patent WO03060163.
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Patent: WO 0242459-A 623 30-MAY-2002;
Sangamo Biosciences Inc. (US)
Location/Qualifiers
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Sequence 623 from Patent WO0242459.
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Sequence 1 from Patent WO0174342.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I bases 1 to 9)
Tsuneyoshi, T., Westerhausen, A., Constantinou, C.D. and Prockop, D.J. Substitutions for glycine alpha 1-637 and glycine alpha 2-694 of type I procollagen in lethal osteogenesis imperfecta. The substitution as be transmitted along the helix introduced by a glycine J. Biol. Chem. 266 (24), 15608-15613 (1991)
                                                                  van Bijk,M.J. and van Schaik,C.
Discrimination and detection of target nucleotide sequences using mass spectrometry
Patent: WO 03060163-A 43 24-JUL-2003;
Keygene N.V. (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenBank staff at the National Library of Medicine created this entry [NCBI glabbg 50583] from the original journal article. This sequence comes from Fig 5A.

Location/Qualifiers
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S50583.1 GI:233928
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100.0%; Pred. No. 4.8e+09;
ative 0; Mismatches 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

August 11, 2004, 15:32:08; Search time 72.2581 Seconds (without alignments) 293.960 Million cell updates/sec Run on:

US-09-540-843-6

1 catac 5 Perfect score: Sequence: ritle:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

3373863 seqs, 2124099041 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200 Minimum DB Maximum DB

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

N\_Geneseq\_29Jan04:\* geneseqn1980s:\* geneseqn1990s:\* Database

geneseqn2001as:\* geneseqn2001bs:\* geneseqn2003as:\* geneseqn2003bs:\* geneseqn2003cs:\* geneseqn2004s:\* geneseqn2002s:\* geneseqn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## A promote GAS compl Oligonucl Direct re Cyclin D Zinc fing Zinc fing Zinc fing Human DNA Melanogen Melanogen Melanogen Melanogen Selection Melanogen Aaz10696 Oligonucl Telomere-Melanogen Oligonucl Oligonucl Telomere-Aca88955 Sell Aaz10694 Oli Aas14911 Mell Acd25826 Mell Acd25822 Tell Aav15899 Cyc Aav15899 Cyc Aav22350 A.p. Aav22283 GAS Description Aaz10695 C Aas14910 M Aas14908 M Acd25823 T Abq71504 Abq71958 Acd25825 Aaz10692 Aas14905 SUMMARIES AAS14910 AAS14908 ACD25825 ACA88955 AAZ10694 AAS14907 ACD25826 AAV15899 AAV22350 AAV22283 AAZ10696 ACD25823 AAS14911 ACD25822 AAZ10692 AAS14905 ABQ71504 Length DB Query Match 1000.0 000000 100.0 100. .00 100. Score 222111431110987483 Result 0 0 0 0 000 000000 0 0 0 0

Ada64249 Zinc fing	Ada62652 Zinc find		Donor			Aaq97224 Oligonucl			Aav50250 Yeast tag		Yeast	Yeast	Aav35934 Primer us	Aav35910 Primer us	Aax18629 p53 seria	Chro	Aaz78624 Human den		Aaz77574 Human den	_	_
ADA64249	ADA62652	ADA64285	AAQ43164	AAQ71104	AAX32625	AAQ97224	AAT35734	AAT66073	AAV50250	AAV50271	AAV50127	AAV50184	AAV35934	AAV35910	AAX18629	AAV73806	AAZ78624	AAZ79270	AAZ77574	AAZ78121	AAZ78625
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## ALIGNMENTS

p53 activity, UV mimetic, UV-irradiation; UV-induced dermatosis; UV-induced hyperproliferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging; Oligonucleotide sequence that increases p53 activity in a cell. AAZ10696 standard; DNA; 5 BP (first entry) skin cancer; ss 23-NOV-1999 AAZ10696; RESULT 1 AAZ10696 

Synthetic.

GB2336157-A

13-0CT-1999

99GB-00006758. 24-MAR-1999;

(UYBO-) UNIV BOSTON

98US-00048927

26-MAR-1998;

Eller Yaar M, Gilchrest BA,

lomere-

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WPI; 1999-543520/46

DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases.

Claim 11; Page 30; 44pp; English

AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are are UV mimetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, and UV-induced dermatoses, reducing photoaging and reducing susceptibility to skin cancer

Sequence 5 BP; 2 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Abq71922 Abx03786 Acd25820

ABQ71922 ABX03786 ACD25820

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Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
                     Melanogenesis associated oligonucleotide #6.
                                                                                                                                                                                                                              Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases.
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                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 p53 activity; UV mimetic; UV-irradiation; UV-induced dermatosis; UV-induced hyperproliferative disease; psoriasis; vitiligo; atopic dermatitis; allergic rhinitis; conjunctivitis; photoaging; skin cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide sequence that increases p53 activity in a cell.
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                         100.0%; Score 5; DB 2; Length 5; 100.0%; Pred. No. 8.5e+08;
                                                                      0; Indels
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                                                 Similarity 100.
5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                              Query Match
Best Local
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AAZ10695/c
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                                                                          Matches
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14-FEB-2002 (first entry)

AAS14910;

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The invention describes inhibition of mammalian epithelial cell

Cr proliferation by treating cells with at least one oligonucleotide, or its

fragment. The compounds, which have cytostatic, anti-allergic, anti-
inflammatory, dermatological, ophthalmological, anti-psoriatic and
immunosuppressive activities, function as 'ultra-violet mimics' to induce

cr inflammatory, dermatological, ophthalmological, anti-psoriatic and
immunosuppressive activities, function as 'ultra-violet mimics' to induce

cr adiation or chemicals, as a proliferation inhibitor, apoptosis inducer

cr a tumour necrosis factor inhibitor. Probably they mimic products of

DNA damage, or processed DNA-damage intermediates, by inducing the p53

cc pathway, resulting in transient arrest of cell growth, allowing more time

cr for DNA repair to occur before cell division takes place. The method is

cr pathway is active states (e.g. psoriasis or precancerous conditions);

reduce photoaging, oxidative stress or damage; prevent skin cancer; treat

allergically mediated inflammation (atopic or contact dermatitis,

allergically mediated inflammation (atopic or contact dermatitis,

allergically mediated inflammation (atopic or contact dermatitis,

cells caused by radiation or chemicals; increase melanin production

cr promote apoptosis in epithelial cells that contain damaged bNA. Also

contignucleotides that contain non-hydrolyzable backbones are used to

contignucleotides used to inhibit mammalian epithelial cell This

contignucleotides used to inhibit mammalian epithelial cell proliferation,

described in the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light.
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                                                                                                                                                                                                                                                                                                                                                                                          Eller M;
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                                                                                                                                                          30-MAR-2001; 2001WO-US010162.
                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540843.
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                                                                                                                                                                                                                                                                                                                                                                                              Yaar M,
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WO200174342-A2.
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                                                                             11-OCT-2001
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AAS14908/c
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Melanin, melanogenic; oligomer; cytostatic; anti-allergic; p53; anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation;
                                                                                conjunctivitis; allergic rhinitis; vitiligo; ss.
                       Melanogenesis associated oligonucleotide #4.
                                                                                                                                              30-MAR-2001; 2001WO-US010162.
                                                                                                                                                              31-MAR-2000; 2000US-00540843.
       14-FEB-2002 (first entry)
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                                                                                                                                                                              (UYBO-) UNIV BOSTON
                                                                                                              WO200174342-A2
                                                                                                                                                                                              Gilchrest BA,
                                                                                                                               11-OCT-2001
                                                                                               Synthetic.
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Eller M;

Yaar M,

The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment. The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, ophthalmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperprobliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (aropic or contact dermatitis, allergically mediated inflammation (aropic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitligg), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This inhibit apoptosis, and allowed the direction of the description of the direction of the data truncated sequence is melanogenesis associated cligonucleotide #4, a truncated version of the oligonucleotide shown in AAS14906, one of the oligonucleotide shown in AAS14906, one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation, Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light. Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 0 Other; described in the method of the invention Claim 1; Page 36; 74pp; English.

.; 0 DB 4; Length 5; Indels ., 8.5e+08; 0; Mismatches 100.0%; Score 5; 100.0%; Pred. No. 5; Conservative Query Match Best Local Similarity Matches 5; Conserv 1 CATAC 5  $\delta$ 

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Gaps

The invention relates to inhibiting growth of cancer cells, which is independent of presence or activity of telomerase in cells, not requiring the presence or activity of p53 normal function in cells, not resulting in S-phase arrest in cells, and inducing apoptosis in cancer cells, which involving administering a composition comprising oligonucleotides which share at least 50% sequence identity with human telomere overhang repeat, (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their contiguous portion) and is used in a method inhibiting proliferation of epithelial cells in a mammal or preventing/reducing DNA damage in cells of a mammal, where the DNA damage is caused by radiation or DNA-damaging chemicals. The method is useful for inhibiting growth of cancer cells chemicals.

Claim 44; Page 6; 65pp; English.

human, promoting differentiation of malignant cells in a mammal, enhancing the expression of one or more surface antigens (e.g. MART-1, tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer cells (especially melanoma cells) in a human and for treatment of other hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis in the skin of a mammal, skin cancer in a human with xeroderma

(especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer, squamous cell carcinoma), for inducing apoptosis in cancer cells in human, promoting differentiation of malignant cells in a mammal,

RESULT 5 ACD25823/c

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Inhibiting growth of cancer cells and inducing apoptosis in cancer cells, by administering composition having oligonucleotides that share sequence identity with human telomere overhang repeat.
                                                                                             Telomere; ss; probe; cytostatic; human; antipsoriatic; dermatological; apoptosis; cancer; p53; epithelial cell proliferation; DNA damage; lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer; squamous cell carcinoma; murface antigen; MRRT-1; tyrosinase; TRP-1; gp-1100; hyperproliferative disorder; spongiosis; blistering; dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis; actinic keratosis; Bowen's disease; basal cell carcinoma; psoriasis; atopic dermatitis; breast cancer; lung cancer; liver cancer; proreatic cancer; brain cancer; bladder cancer; brain cancer; bladder cancer; stomach cancer; brain cancer; ossophageal cancer;
                                                                         Telomere-like oligonucleotide #1 truncated version #2.
                                                                                                                                                                                                                                                                                                                                        /note= "5' phosphorylated"
                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/mod_base= OTHER
ACD25823 standard; DNA; 5 BP.
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31-MAR-2000; 2000US-00540843.
30-MAR-2001; 2001WO-US010162.
                                                (first entry)
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ELLER M S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YAAR M.
                                                                                                                                                                                                                                                                                       Key
modified_base
                                                                                                                                                                                                                                                  Homo sapiens.
                                                 08-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-1996;
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                                                                                                                                                                                                                                                              Synthetic.
                        ACD25823;
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44; Page 3; 65pp; English.
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                                                                                                                                                                                                                                                                                                                      Telomere; ss; probe; cytostatic; human; antipsoriatic; dermatological; apoptosis; cancer; p53; epithelial cell proliferation; DNA damage; lymphoma; oeteosarcome; melanoma; leukaemia; cervical cancer; squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1; gp-1100; hyperproliferative disorder; spongiosis; blistering; dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis; actinic keratosis; Bowen's disoase; basal cell carcinoma; psoriasis; atopic dermatitis; breast cancer; lung cancer; liver cancer;
pigmentosum, seborrheic keratosis, actinic keratosis, Bowen's disease, basal cell carcinoma) and for treating or preventing pre-cancerous conditions affecting epithelial cells (such as psoriasis and atopic
                                dermatitis) and also the types of cancers of breast, lung, liver, prostate, pancreatic, ovarian, bladder, uterine, colon, brain, oesophagus, stomach, and thyroid. The present sequence is a truncated telomere-like oligonucleotide of the invention
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer; uterine cancer; colon cancer; brain cancer; oesophageal cancer; stomach cancer; thyroid cancer.
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                                                                                                                                   0; Indels
                                                                                                               Length 5;
                                                                                                             100.0%; Score 5; DB 8; Le
100.0%; Pred. No. 8.5e+08;
                                                                                        Sequence 5 BP; 1 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                   Telomere-like oligonucleotide #3.
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/note= "5' phospl
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26-MAR-1998; 98US-00048927.
31-MAR-2000; 2000US-00540843.
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                                                                                                                                                                                                                                    ACD25825 standard; DNA; 5 BP.
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                                                                                                  Query Match
Best Local Similarity 100...
5, Conservative
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(YAAR/) YAAR M.
                                                                                                                                                        1 CATAC 5
                                                                                                                                                                              5 CATAC 1
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The invention relates to inhibiting growth of cancer cells, which is independent of presence or activity of telomerase in cells, not requiring the presence or activity of p53 normal function in cells, not requiring sphere in cells, and inducing apoptosis in cancer cells, involving administering a composition comportising oligonucleotides which share at least 50% sequence identity with human telomere overhang repeat, contiguous portion) and is used in a method inhibiting proliferation of epithelial cells in a mammal or preventing/reducing DNA damage in cells of a mammal, where the DNA damage is caused by radiation or DNA-damaging chemicals. The method is useful for inhibiting growth of cancer cells (especially lymphoma, osteosarcoma, melanoma, leukaemia, cervical cancer, and a promoting differentiation of maloran in a mammal, human, promoting differentiation of maloran cells in mammal, human, promoting differentiation of malorance cells in mammal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chancing the expression of one or more surface antigens (e.g. MART-1, tyrosinase, TRP-1 or gp-1100) indicative of differentiation of cancer cells (especially melanoma cells) in a human and for treatment of cancer hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis in the skin of a mammal, skin cancer in a human with xeroderma pigmentosum, seborrheic keratosis, actinic keratosis, Bowen's disease, or basal cell carcinoma) and for treating or preventing pre-cancerous conditions affecting epithelial cells (such as psoriasis and atopic dermatitis) and also the types of cancers of breast, lung, liver, perstate, pancreatic, ovarian, bladder, uterine, colon, brain, opesophagus, stomach, and thyroid. The present sequence is a telomere-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 5; DB 8; Length 5; 100.0%; Pred. No. 8.5e+08; ive 0; Mismatches 0; Indels
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ID ACA88955 standard; DNA; 6 BP.
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12-OCT-2001; 2001AU-00008235.
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Best Local Similarity
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conjunctivitis, and UV-induced dermatoses, reducing photoaging and

Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;

reducing susceptibility to skin cancer

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nucleic acid sequence amplification, for genetic testing or facilitating multiplex PCR amplification from limiting amounts of target nucleic acid. The methods are also useful for improving genetic diagnostic and screening methods, such as prenaral diagnostic testing, foetal sex determination or genetic identification, e.g. DNA profiling or DNA fingerprinting. The nucleic acid sequence amplification is also useful in forensic analysis of degraded, old, ancient and difficult samples that are difficult to amplify and identify. This sequence represents a PCR primer used in the selection and amplification of genetic markers
                                                                                                                                                                                             for nucleic acid sequence amplification comprising selecting each of the genetic markers according to a heterozygosity index of 0.5 or greater. Selecting and amplification of genetic markers are useful as targets for
amplification, useful for improving genetic testing, e.g. fetal sex determination, comprises selecting each of the genetic markers according
                                                                                                                                                                        The invention describes a method of selecting genetic markers as targets
                                                                                                                Claim 36; Page 40; 64pp; English.
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                       DB 7; Length 6; 7.1e+08;
Sequence 6 BP; 2 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
                       Score 5; DB; Pred. No. 7.1 0; Mismatches
                        100.08;
                                    100.08;
                                                5; Conservative
                                   Best Local Similarity
                       Query Match
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CATAC 2 1 CATAC 5

AAZ10694 standard; DNA; 7 BP. (first entry) skin cancer; ss 23-NOV-1999 AAZ10694; RESULT 8 

p53 activity, UV mimetic, UV-irradiation, UV-induced dermatosis, UV-induced hyperproliferative disease, psoriasis, vitiligo, atopic dermatitis, allergic rhinitis, conjunctivitis, photoaging, Oligonucleotide sequence that increases p53 activity in a cell.

GB2336157-A

13-OCT-1999

99GB-00006758 98US-00048927 24-MAR-1999;

26-MAR-1998;

BOSTON (UYBO-) UNIV

Eller M; Yaar M, Gilchrest BA,

DNA fragments useful for increasing p53 activity in a cell and reducing susceptibility to UV-induced hyperproliferative diseases. Claim 11; Page 30; 44pp; English

AAZ10692-97 represent DNA fragments that are used for increasing p53 activity in a cell. The oligonucleotides are are UV mimetics and protect cells against subsequent exposure to UV-irradiation or chemicals. The oligonucleotides are useful for increasing p53 activity in a cell, reducing the susceptibility to UV-induced hyperproliferative diseases, treating psoriasis, vitiligo, atopic dermatitis, allergic rhinitis,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes inhibition of mammalian epithelial cell proliferation by treating cells with at least one oligonucleotide, or its fragment: The compounds, which have cytostatic, anti-allergic, anti-inflammatory, dermatological, obthialmological, anti-psoriatic and immunosuppressive activities, function as 'ultra-violet mimics' to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA repair processes (or a protective response to later exposure to radiation or chemicals), as a proliferation inhibitor, apoptosis inducer or a tumour necrosis factor inhibitor. Probably they mimic products of DNA damage, or processed DNA-damage intermediates, by inducing the p53 pathway, resulting in transient arrest of cell growth, allowing more time for DNA repair to occur before cell division takes place. The method is especially used to treat carcinoma but may also be used to: treat other hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light.
                                        Gaps
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                                        0;
                                        Indels
   Length 7;
 100.0%; Score 5; DB 2; L6 100.0%; Pred. No. 6.1e+08;
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                                      0; Mismatches
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Query Match
Best Local Similarity
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hyperproliferative states (e.g. psoriasis or precancerous conditions); reduce photoaging, oxidative stress or damage; prevent skin cancer; treat allergically mediated inflammation (atopic or contact dermatitis.

allergic rhinitis and conjunctivits); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #3, a truncated version of the oligonucleotide shown in AAS14906, one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation,
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/mod_base= OTHER
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26-MAR-1998; 98US-00048927.
31-MAR-2000; 2000US-00540843.
30-MAR-2001; 2001WO-US010162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Melanin, melanogenic, oligomer, cytostatic, anti-allergic, p53, anti-inflammatory; dermatological; ophthalmological; anti-psoriatic; immunosuppressive; DNA repair; proliferation inhibitor; apoptosis; tumour necrosis factor inhibitor; photoaging; hyperproliferative disease; carcinoma; oxidative stress; skin cancer; allergy mediated inflammation; conjunctivitis; allergic rhinitis; vitiligo; ss.
     allergically mediated inflammation (atopic or contact dermatitis, allergic rhinitis and conjunctivitis); prevent or reduce DNA damage in cells caused by radiation or chemicals; increase melanin production (pigmentation) in epithelial cells (e.g. for treating vitiligo), and to promote apoptosis in epithelial cells that contain damaged DNA. Also oligonucleotides that contain non-hydrolyzable backbones are used to inhibit apoptosis, in response to DNA damage, in epithelial cell. This sequence is melanogenesis associated oligonucleotide #7, one of the oligonucleotides used to inhibit mammalian epithelial cell proliferation, described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inhibiting proliferation of epithelial cells, useful e.g. for treating carcinoma, using specific oligonucleotides that mimic the effects of ultra-violet light.
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                                                                                                                                                                                                                                                                                                           Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CATAC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CATAC 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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AAS14907,

ð g /mod\_base= OTHER /note== "5' phosphorylated"

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0; Mismatches
Best_Local Similarity 100.
Matches 5; Conservative
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CATAC 2
                                   1 CATAC 5
            Matches
                                     ð
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ACD25822 standard; DNA; 7 BP. (first entry) 08-SEP-2003 ACD25822; RESULT 12 ACD25822/c 

Telomere-like oligonucleotide #1 truncated version #1.

Telomere; ss; probe; cytostatic; human; antipsoriatic; dermatological; apoptosis; cancer; p53; epithelial cell proliferation; DNA damage; lymphoma; osteosarcoma; melanoma; leukaemia; cervical cancer; squamous cell carcinoma; surface antigen; MART-1; tyrosinase; TRP-1; gp-1100; hyperproliferative disorder; spongiosis; blistering; dyskeratosis; skin cancer; xeroderma pigmentosum; seborrheic keratosis; actinic keratosis; bowen's disease; basal cell carcinoma; psoriasis; atopic dermatitis; breast cancer; lung cancer; liver cancer; actinic keratosis; prostate cancer; pancreatic cancer; ovarian cancer; bladder cancer; uterine cancer; colon cancer; brain cancer; oesophageal cancer; stomach cancer; thyroid cancer.

sapiens Synthetic Location/Qualifiers /\*tag= a Key modified\_base

28-MAR-2001 (first entry)

AAD02250;

```
The invention relates to inhibiting growth of cancer cells, which is independent of presence or activity of telomerase in cells, not requiring the presence or activity of p53 normal function in cells, not reguling in S-phase arrest in cells, and inducing apoptosis in cancer cells, involving administering a composition comprising oligonucleotides which share at least 50% sequence identity with human telomere overhang repeat, (TTAGG)n. The composition may contain 2 of the oligonucleotides (or their contiguous portion) and is used in a method inhibiting proliferation of a mammal, where the DNA damage is caused by radiation or DNA-damaging of a mammal, where the DNA damage is caused by radiation or DNA-damaging chemicals. The method is useful for inhibiting growth of cancer cells of a mammal, promoting actionama, per indicating apoptosis in cancer cells in cancer in a mammal, are spanned in a mammal, and in a mammal, cervical cancer cells in a mammal, and ferentiation of malignant cells in a mammal, companies, TRP-1 or gp-1100) indicative of differentiation of cancer cells (especially melanoma cells) in a human and for treatment of other hyperproliferative disorders (e.g. spongiosis, blistering or dyskeratosis in the skin of a mammal, skin cancer in a human with xeroderma pignentections affecting epithelial cells (such as psoriasis and acopic conditions affecting epithelial cells (such as psoriasis and acopic deformatitis) and also the types of cancers of breast, lung, liver, prosocate, pancreatic, ovarian, bladder, uterine, colon, brain, cesophagus, scomach, and thyroid. The present sequence is a melanogenic cellomere-like oligonucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
Inhibiting growth of cancer cells and inducing apoptosis in cancer cells, by administering composition having oligonucleotides that share sequence identity with human telomere overhang repeat.
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                                                                                                                                                                                                            Claim 44; Page 18; 65pp; English.
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Inhibiting growth of cancer cells and inducing apoptosis in cancer cells, by administering composition having oligonucleotides that share sequence identity with human telomere overhang repeat.

Yaar M;

Gilchrest BA, Eller MS,

WPI; 2003-512221/48.

26-MAR-1998; 98US-00048927. 31-MAR-2000; 2000US-00540843. 30-MAR-2001; 2001WO-US010162.

(GILC/) GILCHREST B A.

ELLER M S.

(ELLE/)

(YAAR/) YAAR M.

12-APR-2002; 2002US-00122630.

US2003032610-A1.

```
The invention relates to inhibiting growth of cancer cells, which is independent of presence or activity of telomerase in cells, not requiring the presence or activity of p53 normal function in cells, not reguling in C5-phase arrest in cells, and inducing apoptosis in cancer cells, involving administering a composition comprising oligonucleotides which share at least 50% sequence identity with human telomere overhang repeat, (T7AGG)n. The composition may contain 2 of the oligonucleotides (or their contiguous portion) and is used in a method inhibiting proliferation of epithelial cells in a mammal or preventing/reducing DNA damage in cells of a mammal, where the DNA damage is caused by radiation or DNA-damaging chemicals. The method is useful for inhibiting growth of cancer cells of cancer cells in carcinoma), for inducing apoptosis in cancer cells in chuman, promoting differentiation of malignant cells in a mammal, carcinoma), for inducing apoptosis in cancer cells in chuman, promoting differentiation of more more surface antigens (e.g. MART-1, tyrosing the expression of one or more surface antigens (e.g. MART-1, tyrosing the expression of one or more surface antigens (e.g. MART-1, tyrosing the expression of one or more surface antigens (e.g. MART-1, tyrosing the expression of one or more surface antigens (e.g. MART-1, tyrosing the expression of one or more surface antigens (e.g. MART-1, tyrosing the expression of cancer in a human with xeroderma or promoting the expression of cancer in a human with xeroderma propertion and also the types of cancers of breast, lung, liver, conditions affecting epithelial cells (such as psoriasis and atopic demartits) and also the types of cancers of breast, lung, liver, conditions affecting epithelial cells (such as psoriasis and atopic demartities) and also the types of cancers of breast, lung, liver, prosected, prosected, prosected, and thyroid. The present sequence is a truncated conditions affecting epithelial cells in the invention or sequence is a truncated conditions and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7 BP; 3 A; 0 C; 2 G; 2 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 44; Page 6; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD02250 standard; DNA; 8 BP
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Loca 5; Conservative
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cyclin D transcription factor; binding affinity; D-type cyclin; pr cell cycle inhibitor; tumour; detection; cancer; DMP1; competitor;

nonamer consensus sequence; ss.

Homo sapiens. W09743415-A1.

Mus musculus

Cyclin D transcription factor DMP1 nonamer consensus sequence.

26-MAY-1998 (first entry)

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non-integrating viral vector; cytostatic; anti-diabetic; cardiant; neuroprotective; genetic disease; gene therapy; therapy; cancer; cystic fibrosis; diabetes; cardiovascular disease; brain malfunction; genome analysis; chemotherapy; transgenic host cell; direct repeat; ds.
                         Sleeping Beauty; SB; AdSB10; adenovirus; transposase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8 BP; 4 A; 3 C; 0 G; 1 T; 0 U; 0 Other;
      Direct repeat sequence that binds to SB protein.
                                                                                                                                                                                                                                                                                                                 Disclosure, Page 14; 62pp; English.
                                                                                                                                                                         (MINU ) UNIV MINNESOTA.
(BAYU ) BAYLOR COLLEGE MEDICINE.
(MCIV/) MCIVOR R S.
                                                                                                                                     11-MAY-2000; 2000WO-US012827
                                                                                                                                                       99US-0133569P
                                                                                                                                                                                                              (AGUI/) AGUILAR-CORDOVA E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100
les 5; Conservative
                                                                                                                                                                                                                                 Hackett PB,
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Б
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                                                                                                  WO200068399-A2.
                                                                                                                                                       11-MAY-1999;
                                                                                Unidentified
                                                                                                                   16-NOV-2000.
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                                                                                                                                                                                                                                                                                                malfunction
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Aguilar-Cordova E;

Cyclin D transcription factor and related DNA - can be used to develop products for treatment of, e.g. cancer.

(SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

Sherr CJ,

Hirai H,

WPI; 1998-008884/01.

96US-0017815P. 96US-00648837. 97WO-US008480.

16-MAY-1996; 16-MAY-1996;

15-MAY-1997;

16-MAY-1997;

20-NOV-1997.

97US-00257071

```
This is a nonamer consensus sequence of a cyclin D transcription factor DMP1. DMP1 is an amino acid polymer which has binding affinity for a D-c type cyclin, in vitro, and for a specific DMA nuclectide sequence and is a transcription factor involved in the activation of genes that prevent cell proliferation. The DMP1 nucleic acid is operatively linked to an expression control sequence in an expression vector. The expression control sequence comprising this nonamer ceptor has a transcription control sequence comprising this nonamer ceptor as a transcription control sequence comprising this nonamer ceptor in a chromosome of a transgenic animal. A probe or a cassette insertion site for a recombinant gene. The vector is homologously recompetitor in DMP1 transactivation assays is designed based on this competitor in DMP1 transactivation assays is designed based on this competitor in DMP1 transactivation assays is designed based on this companied in a chromosome of a transgenic animal. A probe or a competitor binding of DMP1 as probe to DMP1 as probe to DMP1 where the probe under conditions that allow binding of the probe under conditions that allow binding of the probe contains the core sequence GTA, and where the probe to DMP1 is suspected in the sample. DMP1 can concentraling the expression of DMP1 can be used to treat tumours and other concented. The presence or activity of DMP1 can be used to treat tumours and other concented by the probes of DMP1 in cells is useful for detection of cancer cells or inhibit can detection of cancer cells or inhibit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 99; 120pp; English.
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AAV22350/c
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The parent calsoloses in-inceptants that bind a transposase, a transposase-encoding polynucleotide operably linked to a regulatory sequence comprising an operator, that alters expression of the response encoding polynucleotide. Transposon sequences can integrate transposase-encoding polynucleotide. Transposon sequences can integrate into genomic DNA whether or not the cell is dividing. AdSB10 is a SB (Sleeping Beauty) transposase-transducing adenoviral non-integrating of vector. The non-integrating viral vectors are useful for treating genetic disease characterised by subnormal production of a polypeptide or RNA, or supplementation of a metabolic activity. These genetic diseases include cystic fibrosis, diabetes, cardiovascular disease, cancer or nucleic acid delivery systems, e.g. for genome analysis or gene therapy and can also be used for applications that involve long-term production of a polypeptide. The non-integrating viral vectors are also useful for creating transgenic host cells that provide normal cells with protection against toxic side effects of chemocherapy. The sequence of the present invention is a direct repeat sequence that binds to SB protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-integrating (adenovirus-based) viral vectors useful in gene therapy, especially for treating patients suffering from a genetic disease, e.g. cystic fibrosis, diabetes, cardiovascular disease, cancer or brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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100.0%; Pred. No. 5.3e+08;
tive 0; Mismatches 0;
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Gaps

.; 0

AAV22350;

AAV15899 standard; DNA; 9 BP.

AAV15899

RESULT 14
AAV15899/C
ID AAV158:
XX
AC AAV158:
XX

1 CATAC 5

à

Best Loc Matches

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3' untranslated region; UTR; inhibition; gene expression; ICAM-7; interferon-gamma; IFN-gamma; major histocompatibility complex; MHC; antigen expression; gene promoter; utron; B7-1; B7-2; Fc gamma R; HIV gene expression; transplant rejection; treatment; autoimmune disease; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a promoter regulatory element, found in the utrons of the invention. Utrons are from, or are homologous to, the 3' untranslated region (UTR), of an mRNA that stimulates or inhibits a cellular response by sequence specific interactions. The utron is able to suppress constitutive and interferon-gamma (IFN-gamma) induced major histocompatibility complex (MHC) class I and class II antigen expression and expression of other antigens, the gene promoters of which contain related sequence motifs that are stimulated by the same factors which stimulate MHC class I and class II antigen expression. Such utrons can be used to regulate gene expression in a subject, e.g. a human or a cell in vitro, specifically inhibiting MHC Class I or II, ICAM-7, B7-1, B7-2, FC gamma R, IL-2 or HIV gene expression. They can be used to inhibit transcribant rejection, or treat an autoimmune or inflammatory disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Utrons, RNA molecules containing promoter regulatory motifs - useful to suppress express expression from promoter of interest, specifically TSU nucleic acid suppression of MHC Class I and II gene expression.
                                        A promoter regulatory motif found in the utrons of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 20; 200pp; English
                                                                                                                                                                                                                                                                                                                                     97WO-US009459.
                                                                                                                                                                                                                                                                                                                                                                            96US-00646789
29-JUN-1998 (first entry)
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                                                                                                                                                                                                                                                                                        27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peyman JA;
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SQ Sequence 9 BP; 3 A; 0 C; 3 G; 0 T; 3 U; 0 Other;

Query Match
Best Local Similarity 100.0%; Pred. No. 4.7e+08;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

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1 CATAC 5

5 CATAC 1

Search completed: August 11, 2004, 17:56:32 Job time: 76.5914 secs

(OIGSU) AMOIS BEDA 2141

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AZ434551 AZ464990 AZ486152 AZ579566 AZ579566

AZ626685 AZ645469 AZ647364 AZ759906 AZ766086 AZ799396 AZ815067

AZ864822 AZ942806

AA977115 AI120725 AI747751 BX551013

AZ345849 AZ355195 AZ406137 AZ422163

AI721735 BG928185 BG929060 BQ595683

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13 bp mRNA linear EST 22-SEP-2003
024-030-D02 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, Caryophyllales, Amaranthaceae, Beta.

(hases 1 to 13)
Herwag,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,W., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                CF543283.1 GI:34891723
EST.
Beta vulgaris
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                     27513289 seqs, 14931090276 residues
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gb_htc:*
gb_htc:*
gb_est2:*
gb_est4:*
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em_gss_hum:*
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Maximum DB seq length: 200
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ALIGNMENTS

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100.0%; Score 5; DB 12; L
100.0%; Pred. No. 3.7e+06;
ive 0; Mismatches 0;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2102843"
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                                                                                                                                                                                                                                                                            /tissue_type="leaf"
/lab host="EMDH10B"
/clone_lib="MPDH10B"
/clone_lib="MPDH2ADIS-024-leaf"
/note="Vector: pcWVSPORT6; Site_1: SalI; Site_2: NotI;
/note="Vector: pcWVSPORT6; Site_1: SalI; Site_2: NotI;
/note="Vector: pcWVSPORT6; Site_1: SalI; Site_2: NotI;
/note="Vector: pcWVSPORT6; Site_2: NotI;
/note="Vector: pcWVSPORT6; Site_2: NotI;
/note="Vector: pcWVSPORT6; Site_2: NotI;
/note_2: SalI-NotI; primer sites and
/note_2: SalI-NotI; primer sites and
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/clone lib="Chilcoat/furkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
                                                                                                                                                                                                                                                                                                                                                                                                                          orientation:
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
SP6-SalI-CCACGCGTCCG-Sprime-cDNA-polyA-CC-NotI-T7;
Spequencing granted in the context of the GABI-Beet
project, local P1: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 14)

Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
                                                                                                                                                      /mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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5009-0-42-D11.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
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Eukaryota, Alveolata, Ciliophora, Oligohymenophorea,
Hymenostomatida, Tetrahymenina, Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 13; 3.7e+06;
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University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Brror: 0.00
Plate: 30 row: D column: 02
Seg primer: SP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                     organism="Beta vulgaris"
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db_xref="taxon:161934"
clone="024-030-D02"
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/strain="CU428.1"
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Matches 5; Conserv
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                            A1424037 16 bp mRNA linear EST 09-MAR-1999 tf51h06.xl NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2102843 3' similar to TR:Q69566 Q69566 ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NCI/NINDS-CAGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 3.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trace considered overall poor quality
Seg primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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stage embryos."

[Jab_host="Xboante embryos, adult livers, snield stage embryos"

[Jab_host="XL1-blue MRF"]

[Aloo | Lib="Zebrafish Washu MPING EST"]

[Aloo | Lib="Zebrafish Washu MPING EST"]

[Aloo | Lib="Yearly repeated to Sal | Ladaptors | Lib Strand cDNA was pined with a Not I - oligo(dT) is primer | Extrand cDNA was ligated to Sal I adaptors (BEL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORTI vector (BEL). Library was constructed by Matthew Clark (Lehrach lab, ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). London and Max Planck Institut fuer Molekulare Genetik, Berlin). CDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster CDNAs, and a single cDNA from each cluster were sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones
Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

E 1 (bases 1 to 16)

S Clark, M. Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Bddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish EST Project 1998

Unpublished (1998)

Unpublished (1998)

Cother ESTs: fc31908 v.1

Contact: Stephen L. Johnson
Washington University School of Medicine
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800

Fax: 314 286 1810

Email: zbratish@watson.wustl.edu

Email: zbratish@watson.wustl.edu

Email: zbratish@watson.wustl.edu

Email: zbratish@watson.wustl.edu

Matthew Clark. DNA Sequencing by: Washington University Genome

Sequencing Center Clone distribution: Genome Systems, St. Louis,

Missouri (web address: www.genomesystems.com) (email contact:

Info@genomesystems.com) and Research Genetics, Huntsville, Alabama

(web address: www.resgen.com) (email contact: info@resgen.com) and

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="26 somite embryos, adult livers, shield
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seg primer: T7 ET from Amersham
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/db_xref="taxon:7955"
/clone="IMAGE:3723038"
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Location/Qualifiers
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BG928185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E, Consortium/LLNL at:
                           AI685758

16 bp mRNA linear EST 27-MAY-1999
tu37909.X1 NCI_CGAP_Pr28 Home sapiens cDNA clone IMAGE:2253280 3'
similar to TR:Q02393 Q02393 HUMAN PAPILLOMAVIRUS 18 ES CENTRAL
SEQUENCE MOTIF PROTEIN 1; contains element LTR4 repetitive element
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                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seg primer: -400P from Gibco
High quality sequence stop: 1.
Location/Qualifiers
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/lab host="DH10B"
/clone lib="NCI CGAP Pr28"
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/db_xref="taxon:9606"
/clone="IMAGE:2253280"
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AI721735.1 GI:5040064
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Unpublished (1997)
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BQ595683.1 GI:26125266
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HNC11-1-G8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
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EST 06-NOV-2001
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Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
                                                                                                                                                                          1 (bases 1 to 16)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
                                                                                                                                                                                                                                                                                                                                                                                     GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: 610-270-5598
Seq primer: 177
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 17)
                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
BG928185 16-NOV-
HNC65-1-D12.R.R HNC (Human Normal Cartilage) Homo sapiens CDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab host="s.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: Sall; Site_2: NotI;
                                                                                                                                                                                                                                          Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001)
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100.0%; Pred. No. 3.8e+06;
iive 0; Mismatches 0;
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                                                                     BG928185.1 GI:14322708
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UW2109
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Homo sapiens
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Best Local Similarity 100...
                                    mRNA sequence.
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BQ595683
E012692-024-022-H17-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
cDNA clone 024-022-H17 5-PRIME, mRNA sequence.
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1 (Bases I to 17)

1 (Bases I to 17)

Drungowski, M., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
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/tissue_type="developing root"
/lab host="MPDILOB"
/clone_lib="MPIZ-ADIS-024-developing root"
/clone_lib="MPIZ-ADIS-024-developing root"
/clone_lib="MPIZ-ADIS-024-developing root"
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/clone_lib="MPIZ-ADIS-024-developing root"
/clone_lib="MPIZ-ADIS-02"
/clone_lib="MPIZ-ADIS-03"

GlaxoSmithKline
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719 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
710 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Fax: 610-270-5598
Email: sanjay kumar-1@gsk.com
Seq primer: 177
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/culTivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo mapiens"
/mol Lype="mmNA"
/db zref="teaxon:9606"
/tissue_type="cartilage"
/lab.host="R.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: Sall; Site_2: NotI;
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ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 22 row: H column: 17
Seg primer: SP6; CATACGATTTAGGTGACACTATAG.
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/db_xref="taxon:161934"
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AA977115 19 bp mRNA linear EST 26-MAY-1998 og24c08.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1587278 3' similar to TR:Q69566 Q69566 ;, mRNA sequence.
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Emmetr-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Tetrahymena thermophila"
/mol type="mRNA"
/mol type="mRNA"
/strain="1641248.1"
/db xref="taxon:591"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Yector: BluesGriptz SK*, Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                       Tetrahymena thermophila

Bukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 18)

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,

Frankel, J. and Klobutcher, L.

BST from Tetrahymena thermophila, strain CU428.1, growing cells
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                                                                                                                                                                                                                                                                              University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
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Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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                                                                                                                                                                                                  Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
                                                                                                                                                                                                                                                                                                                                                                               Email: apturkew@midway.uchicago.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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     Tetrahymena thermophila
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AA977115.1 GI:3154561
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Best Local Similarity 10v...
5, Conservative
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b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
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                                                 Note:
                                                                    Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung: Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1-3, Yamada-Oka, Suita, Osaka Pref. 565, Japan

Tel: 06-877-511(ex.315)

Email: kousaku@imcD.osaka-u.ac.jp

Me are not submitting the same cDNA sequence redundantly to DDBJ

since 1993. For the abundance information of clones with this

sequence in this library and as well as in other 3'-directed

libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The

sequences of the clones represented by this GS sequences is also

found there.
                                                                                                                                                                                                                                                                                Gaps
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dev_sreg="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
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BodyMap, human gene expression database
Unpublished (1995)
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AUTHORS

FEATURES

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EST 22-JUN-1999

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/dev stage="embryo, 14 dpc"
/lab_host="number of the color of the colo
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Marxa,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse BST Project 1999
Unpublished (1999)
ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI74751 19 bp mRNA linear EST 22-Jul19105.x1 Sugano mouse embryo mewa Mus musculus CDNA clone LIMAGE:2088249 3' similar to TR:P79101 P79101 CLEAVAGE AND POLYADDENYLATION SPECIFITY FACTOR PROTEIN: ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: Similarity on wrong strand Seq primer: custom primer used High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                             100.0%; Score 5; DB 9; Length 19; 100.0%; Pred. No. 3.8e+06;
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/mol_type="mRNA"
/strain="C57BL"
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/clone="IMAGE:2088249"
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/tissue type="mammary gland"
/lab_host="DH10B"
/clone lib="Soares mammary gland NMLMG"
/clone lib="vector: pT733-Pac (Pharmacia) with a modified
/note="Vector: pT773-Pac (Pharmacia) with a modified
/note="vector: pT733-Pac (Pharmacia) with a modified
/note: pT733-Pac (Pharmacia) w
                                                                                        /tissue type="pooled germ cell tumors"
/lab_host="DH10B"
/lab_host="DH10B"
/clone_lib="NGI_CGAP_GG4"
/note="Vector: pT713D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Marra,M., Hillier,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Contact: Marra W/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
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Sossible reversed clone: Similarity on wrong strand
Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 5; DB 9; Length 19; 100.0%; Pred. No. 3.8e+06; ive 0; Mismatches 0; Indels
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The WashU-HHMI Mouse EST Project
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/db_xref="taxon:10090"
/clone="IMAGE:1383261"
                       /db_xref="taxon:9606"
/clone="IMAGE:1587278"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:37546"
/clone="reall6al2 qlc"
/tiscue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
                                                       Gaps
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(bases 1 to 19)
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Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
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             100.0%; Score 5; DB 9; Length 19; 100.0%; Pred. No. 3.8e+06; ive 0; Mismatches 0; Indels
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7. organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
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Genome Biol. 4 (10), R63 (2003)
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Glossina morsitans morsitans
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Pathogen Sequencing Unit
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
We are not submitting the same cDNA sequence redundantly to DDBJ
since 1933. For the abundance information of clones with this
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka- u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also
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/db_xref="taxon:9606"
/db_ztage="adult"
/clone lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"
                                                                                                                                                                                                                                                                                                                                                                                                                              1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
                                                                                                                                                                                                                                                                                                                                                               Institute for Molecular and Cellular Biol
                                                                                                                                                                                                                                                           BodyMap; human gene expression database
Unpublished (1995)
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/organism="Homo sapiens"
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Job time : 607.215 secs
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C00646.1 GI:1432876
                                                                 Homo sapiens (human)
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(otasu) Andla elepa siat

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623, App
2220, Ap
2256, Ap
37, Appl
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Sequence 4, Appli
                                                                                            August 11, 2004, 17:57:26; Search time 15 Seconds (without alignments) 184.984 Million cell updates/sec
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Sequence 12,
Sequence 3, 7
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-989-789-2220
US-09-989-789-2256
US-09-721-777-19
US-08-35-55-5A-27
US-08-232-233-1
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US-09-048-927-4
US-09-498-851-20
US-08-615-170-10
US-08-615-170-12
US-09-048-927-3
US-09-142-593-11
US-09-927-886-17
US-08-646-789A-8
US-08-646-789A-8
US-08-646-789A-8
US-08-646-789A-8
US-08-646-789A-8
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US-08-351-748-25
US-08-202-927-25
US-08-430-536A-23
US-08-430-536A-23
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                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-319-648-68
US-09-989-789-623
                                                                                                                                                                                                                                                                                         682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                     IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                  US-09-540-843-6
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Match Length
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Maximum DB seq length: 200
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Perfect score
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Sequence 45, Appl	Sequence 1, Appli	Sequence 23, Appl	Sequence 25, Appl	Sequence 174, App	Sequence 174, App	Sequence 45, Appl	Sequence 24, Appl	Sequence 33, Appl	Sequence 1, Appli	Sequence 30, Appl	Sequence 31, Appl	Sequence 174, App	Sequence 1, Appli	Sequence 174, App	Sequence 23, Appl	Sequence 34, Appl	Sequence 7, Appli
US-08-171-718-45	US-08-703-601-1	US-08-684-547-23	US-08-684-547-25	US-08-469-318-174	US-08-468-609A-174	US-08-478-087-45	US-09-063-450-24	US-09-063-450-33	US-09-123-638-1	US-08-646-695-30	US-08-875-533-31	US-08-446-872A-174	US-09-724-753-1	US-08-762-227A-174	US-09-475-947A-23	US-09-427-834A-34	US-09-445-388A-7
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ALIGNMENTS

RESULT 1  Sequence 20, Application US/08855372B  Sequence 20, Application US/08855372B  Patent No. 6090549  GENERAL INFORMATION:  APPLICANT: Parinov, Andrei D  APPLICANT: Parinov, Sergei V  APPLICANT: Rivillov, Eugene V  APPLICANT: Rivillov, Eugene V  APPLICANT: Dubiley, Svetlana A  TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as of TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as of TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as of TITLE OF INVENTION: Use of Continuous/Contiguous Stacking Hybridization as of TITLE OF INVENTION Reacher Drive  COUNTRY: United States  STATE: 111inois  COUNTRY: United States  COMPUTER READABLE FORM:  MEDIUM TYPE: 3.50 inch, 1.4 MB storage  COMPUTER: PC  COMPUTER: PC  OPERATING SYSTEM: Microsoft Windows 98  SOFTWARE: Wordperfect  CURRENT APPLICATION DATE:  FILING DATE: 13-MAY-97  FILING DATE: 13-MAY-97	PRIOR APPLICATION DATA: APPLICATION NUMBER: U.S. 08/587,332 FILING DATE: 16-DAN-96 ATTORNEY, AGENT INFORMATION: NAME: Cherskov, Michael J. REGISTRATION NUMBER: 33,664 REFERENCE/DOCKET NUMBER: ANL-IN-95-027 TELECOMMUNICATION INFORMATION:
30 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0	- 1- 1- 1- 1- 1- 1- 1-

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Gaps 0;

Query Match

100.0%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+00;
Matches 5; Conservative 0; Mismatches 0; Indels

TYPE: nucleic acid
STRANDEDNESS: No. 6090549 Applicable
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: yes

US-08-855-372B-20

TELEPHONE: (312) 621-1330

TELEFAX: (312) 621-088
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 5 bases

Diagn

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HYPOTHETICAL: yes
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APPLICANT: ORDAHL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                 US-09-498-851-20
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APPLICANT: Mirzabekov, Andrei D
APPLICANT: Parinov, Sergei V
APPLICANT: Barsky, Victor E
APPLICANT: Mirillov, Eugene V
APPLICANT: Dubiley, Svetlana A
TITLE OF INVENTION: Use of Continuous/Contiguous
TITLE OF INVENTION: Stacking Hybridization as a Diagnostic Tool.
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHERSKOV & FLAYNIK
STREET: 20 N. Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Yaar, Mina
APPLICANT: Eller, Mark
FILE REFERENCE: BU94-68A2
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT PAPLICATION NUMBER: 08/952,697
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTERQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 5; DB 3; Length 5; 100.0%; Pred. No. 1e+08; ative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 inch, 1.4 MB storage
Assumpte: PC Microsoft Windows 98
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CURRENT APPLICATION DATA:
PRILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/855,372
APPLICATION NUMBER: 08/855,372
FILING DATE: 13-MAY-97
APPLICATION NUMBER: U.S. 08/587,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/09498851
Patent No. 6440671
                                                                                                                               Sequence 4, Application US/09048927
Patent No. 6147056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: DNA Fragment
US-09-048-927-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
STATE: Illinois
COUNTRY: United States
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Best Local Similarity 100..
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                              CATAC 1
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US-09-498-851-20/c
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MAR, Janet H.
APPLICANT: FARRANCE, Iain K.G.
APPLICANT: HALL, Deborah E.
APPLICANT: STEMART, Alexandre F.R.
APPLICANT: STEMART, Sarah B.
TITLE OF INVENTION: DIEF-1 ISOFORMS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY. San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
FILING DATE: 16-JAN-96
ATTORNEY/AGENT INFORMATION:
NAME: Cherskov, Michael J.
REGISTRATION NUMBER: 33,664
REFERENCE/DOCKET NUMBER: ANL-IN-95-027
TELECOMMINICATION INFORMATION:
TELEPHONE: (312) 621-088
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     LENGTH: 5 bases
TYPE: nucleic acid
STRANDEDNESS: No. 6440671 Applicable
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APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILLING DATE: 06-FEB-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-615-170-10
; Sequence 10, Application US/08615170
; Patent No. 5776776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORDAHL, Charles P. AZAKIE, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFRA: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Sequence 11, Application US/09142593

Patent No. 6489458

Patent No. 6489458

PAPLICANT: HACKETT ET AL.

TITLE OF INVENTION: INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: MUETING, RAASCH & GEBHARDT, P.A.
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APPLICANT: Gilchest, Maria
APPLICANT: Eller, Maria
APPLICANT: Eller, Maria
TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: BU94-68A2
CURRENT APPLICATION WUMBER: US/09/048,927
CURRENT FILING DATE: 1996-03-26
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER FILING DATE: 1996-06-03
EARLIER FILING DATE: 1996-06-06
NUMBER OF SEQ ID NOS: 4
                                         100.0%; Score 5; DB 1; Length 7; 100.0%; Pred. No. 7.4e+07;
                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 5; DB 3; Length 7; 100.0%; Pred. No. 7.4e+07; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                          0; Mismatches
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119 NORTH FOURTH STREET, SUITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Polocial
                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09048927
Patent No. 6147056
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: DNA Fragment US-09-048-927-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MINNEAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MINNESOTA COUNTRY: USA
                                                                                                                                                                                                                            1 CATAC 5
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       MOLECULE TYPE:
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                                                                                                                                                                                                                                   100.0%; Score 5; DB 1; Length 7; 100.0%; Pred. No. 7.4e+07; Live 0; Mismatches 0; Indels
                                                                                                                     DIEF-1 ISOFORMS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Heslin, James M.
REGISTRATION UNDBER: 29,541
REFERENCE/DOCKET NUMBER: 2307U-053120
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAR, Janet H.,
FARRANCE, Iain K.G.
HALL, Deborah E.
STEWART, Alexandre F.R.
LARKIN, Sarah B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION: DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08615170 Patent No. 5776776 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORDAHL, Charles P. AZAKIE, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
SEQUENCE CHARACTERISTICS:
                                   nucleic acid
                  7 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: STEWART, APPLICANT: LARKIN, SA TITLE OF INVENTION: D NUMBER OF SEQUENCES:
                                                                      linear
                                                                                       MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RY: US
94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 0. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                          1 CATAC 5
                                 TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                          1 CATAC 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                               US-08-615-170-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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APPLICANT: Michonagh, Kevin T.
APPLICANT: Michhuis, Arthur
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 5; DB 2; Length 9; 100.0%; Pred. No. 5.8e+07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08646789A
Patent No. 6022863
GENERAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: FENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
FILING DATE: 31-0CT-1994
APPLICATION NUMBER: 07/887,712
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPPRATING SYSTEM: PC-DOS
                                                             RESULT 9

18-08-583-276-1/c

18-09-883-276-1/c

Sequence 1, Application US/08583276

Patent No. 5837536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DESCRIPTION: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: singular
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Best Local Similarity 100.
Matches 5; Conservative
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RY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 9 bases
                                                                                                                                                  GENERAL INFORMATION:
CATAC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-646-789A-8/c
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APPLICANT: Kay, Mark A.
APPLICANT: Kay, Mark A.
APPLICANT: Kay, Mark A.
APPLICANT: Yau, Stephen
TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a
TITLE OF INVENTION: Sleeping Beauty Transposon System
TITLE OF INVENTION: Sleeping Beauty Transposon System
FILE REFERENCE: STAN. 160CLP
CURRENT APPLICATION NUMBER: US/09/927,886
CURRENT APPLICATION NUMBER: 60/162,279
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-17
NUMBER OF SEQ ID NOSE: 1999-11-17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 5; DB 4; Length 8; ilarity 100.0%; Pred. No. 6.5e+07; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

100.0%; Score 5; DB 4; Length 8;

Best Local Similarity 100.0%; Pred. No. 6.5e+07;

Matches 5; Conservative 0; Mismatches 0; Indels
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US-09-927-886-17
                                                                                    PULING APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/40,664
FILING DATE: 11-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/053,868
FILING DATE: 28-70L-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/065,303
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/065,303
FILING DATE: 11-MAR-1998
APPLICATION NUMBER: PCT/US98/04687
FILING DATE: 11-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REGISTRATION NUMBER: 110.00450101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1226
    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,593
FILING DATE: 10-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 17, Application US/09927886
Patent No. 6613752
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: DNA (genomic) US-09-142-593-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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Best Local Similarity
Matches 5; Conserv
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                                                  FILING DATE: 1 CLASSIFICATION:
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US-09-927-886-17
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LENGTH: 8
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100.0%; Score 5; DB 3; Length 9; 100.0%; Pred. No. 5.8e+07;
                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                         ; Sequence 1, Application US/09048927; Patent No. 6147056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: DNA Fragment US-09-048-927-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
            Query Match
Best Local Similarity 100.00
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                  1 CATAC 5
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                                                                                                                                                                                                                                        US-09-048-927-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
LENGTH: 9
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: May 21, 1996
CLASSIFICATION: 800
ATTORNEY/AGRIT INFORMATION:
NAME: Misrock, S. Leslie
REGISOFRATION NUMBER: 18,872
REFRENCE/DOCKET NUMBER: 6523-006
TELECOMMUNICATION INFORMATION:
TELEFRANCE (212) 790-9090
TELEFRANCE (212) 790-9090
TELEFRANCE (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:

COUNTRY:

ZIP: 10036-2711

COMPUTER READBLE FORM:

MEDITOW TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OFFRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATEMIT Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION: 800

CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-646-789A-80/c
Squence 80, Application US/08646789A
Fatent No. 6022863
SAFERAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
WUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 5; DB 3; Le Best Local Similarity 100.0%; Pred. No. 5.8e+07; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6523-006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 65,77
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATAC 1
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Sequence 68, Application US/09319648
Patent No. 6451530
GENERAL INFORMATION:
TITLE OF INVENTION: Fluorescent Nucleotide Analog Hairpin
Formation for Detection of Nucleic Acid Hybridization
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Gaps
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                                                                                                                                                                                                                                                                                                          APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Mina
APPLICANT: Bler, Mark
TITLE OF INVENTION: Use of Locally Applied DNA Fragments
FILE REFERENCE: BU94-68A2
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT APPLICATION NUMBER: US/09/048,927
CURRENT FILING DATE: 1996-06-03
EARLIER APPLICATION NUMBER: 08/952,697
EARLIER PILING DATE: 1996-06-03
EARLIER FILING DATE: 1996-06-03
EARLIER FILING DATE: 1996-06-03
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 5; DB 3; Length 9; 100.0%; Pred. No. 5.8e+07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/319,648
FILING DATE: 30-Jul-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US 60/032,844
FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Embarcadero Center, Eighth Floor
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1 CATAC 5
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8 CATAC 4
    LENGIH: 9
                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2220, Application US/09989789
Patent No. 6588746
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REPERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/09/989,789
CURRENT FILING DATE: 2002-03-25
NUMBER: OF SEQ ID NOS: 4085
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 623, Application US/09989789

Patent No. 6588746

GENERAL INFORMATION:

TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REPERENCE: 8325-0011.20 / S11-US2

CURRENT APPLICATION NUMBER: US/09/989,789

CURRENT FILING DATE: 2002-03-25

NUMBER OF SEQ ID NOS: 4085

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 5; DB 4; Length 9; 100.0%; Pred. No. 5.8e+07;
                                                                                    REFERENCE/DOCKET NUMBER: 48,631
REFERENCE/DOCKET NUMBER: 015280-288100US
REFERENCE/DOCKET NUMBER: 015280-288100US
TELEPHONE: (415) 576-020
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHRACTERISTICS:
LENGTH: 9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FOPPLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
APPLICATION NUMBER: WO PCT/US97/22448 FILING DATE: 10-DEC-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                             NAME: Fang, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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US-09-989-789-2220/c
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US-09-989-789-623
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CORGANISM: Artificial Sequence
CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: example target
COTHER INFORMATION: DNA
US-09-989-789-2220

QUETY MATCH

Best Local Similarity 100.0%; Score 5; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.8e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 1 CATAC 5

DD 8 CATAC 4

Search completed: August 11, 2004, 19:33:23
Job time: 17 secs
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August 11, 2004, 19:00:04; Search time 72:0968 Seconds (without alignments) 340.279 Million cell updates/sec
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| Cgn2_6/ptodata/2/pubpna/US07 PUBCOMB seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBF PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBF PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US06_PUBFOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/2/pubpna/US09_RW_PUB.seq:*
| Cgn2_6/ptodata/2/pubpna/US00_RW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                       OM nucleic - nucleic search, using sw model
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Perfect score:
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                                                                                                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 4, Appli	Sequence 4. Appli	. 6	Sequence 178029,	Sequence 178043,	Sequence 3. Appli	Sequence 7, Appli	m	7	178	Sequence 178043,	Sequence 11, Appl	Sequence 17, Appl
SUMMARIES	US-10-122-630-4	US-10-122-633-4	US-10-122-633-6	US-10-027-632-178029	US-10-027-632-178043	US-10-122-630-3	US-10-122-630-7	US-10-122-633-3	US-10-122-633-7	US-10-027-632-178029	US-10-027-632-178043	US-09-142-593-11	US-09-927-886-17
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US-09-861-014-6	US-10-314-578-1138	4	- 1	US-10-191-698-11	US-10-332-914-5	-608-516-	US-09-989-789-623	US-09-989-789-2220	US-09-989-789-2256	US-09-990-186-623	-60-		US-09-989-994-623	US-09-989-994-2220	-989-994-2	US-10-122-630-1	US-10-122-633-1	US-10-096-596-32	US-10-378-558A-13	US-10-427-629-3	US-08-935-377-16	US-09-822-250-16	US-09-398-399-31	US-09-989-789-622	US-09-989-789-636	US-09-989-789-1338	US-09-989-789-1341	US-09-989-789-1342	US-09-989-789-1343	US-09-899-381-31
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## ALIGNMENTS

US-10-122-630-4/c

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USECULO LAZE 30.4-(7)

Sequence 4, Application US/1012630

SEQUENCE IN PROPRIATION:

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Gilchrest, Barbara A.

APPLICANT: Bler, Mark S.

TITLE OF INVENTION: Method to Inhibit Cell Growth Using

TITLE OF INVENTION: Oligonuclectides

TITLE OF INVENTION: Oligonuclectides

FILE REFERENCE: 0054-1088-018

CURRENT APPLICATION NUMBER: US/10/122,630

CURRENT FILING DATE: 1095-06-06

PRIOR FILING DATE: 1095-06-06

PRIOR PELLOR NUMBER: PCT/US96/08386

PRIOR PELLOR NUMBER: US 09/448,927

PRIOR PELLOR DATE: 1098-03-26

PRIOR PELLOR DATE: 2001-03-31

PRIOR PELLOR DATE: 2001-03-31

PRIOR PELLOR DATE: 2001-03-31

PRIOR PELLOR DATE: 2001-03-31

PRIOR PELLOR DATE: SO01-03-31

PRIOR PELLOR DATE: PRIOR WINDER: PCT/US01/10162

PRIOR PELLOR DATE: SO01-03-31

PRIOR PELLOR DATE: PRIOR DATE: PRIOR PELLOR DATE: PRIOR PELLOR DATE: PRIOR DATE: PRIO
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Length 5;

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100.0%; Score 5; DB 15; I
100.0%; Pred. No. 9.4e+08;
ive 0; Mismatches 0;
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             Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
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US-10-122-633-6
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Sequence of Application US/10122633

Seneral No. US2003002611A1

GENERAL INFORMATION:

APPLICANT: Glichrest, Barbara A.

APPLICANT: Blex, Mark S.

APPLICANT: Blex, Mark S.

TITLE OF INVENTION: Method to Inhibit Cell Growth Using TITLE OF INVENTION: Oligonucleotides

FILE REFERENCE: 0054.1088-019

CURRENT PILING DATE: 2002-04-12

PRIOR PILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2001-03-30

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 4

LENGTH: 5

LENGTH: 5
                                                                                                                                   US-10-122-530-6

US-10-122-530-6

Sequence 6, Application US/10122630

Publication No. US20030032610A1

GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Mark S.
TITLE OF INVENTION: Mothod to Inhibit Cell Growth Using TITLE OF INVENTION: Mothod to Inhibit Cell Growth Using FILE REFERENCE: 0054.1088-018

CURRENT APPLICATION WIMBER: US/10/122,630

CURRENT APPLICATION NUMBER: US 08/467,012

PRIOR PILING DATE: 1995-06-06

PRIOR PILING DATE: 1995-06-06

PRIOR PILING DATE: 1995-06-05

PRIOR PILING DATE: 1996-06-03

PRIOR PILING DATE: 1996-06-03

PRIOR PILING DATE: 1998-06-03

PRIOR PILING DATE: 1998-06-03

PRIOR PILING DATE: 1998-06-03

PRIOR FILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 2001-03-31

PRIOR PILING DATE: 2001-03-31

SEQ ID NO SEQ ID NOS: 15

LENGTH: 5

LENGTH: 5
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FEATURE:
OTHER INFORMATION: Synthetic DNA Fragment
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Best Local Similarity 100.
Matches 5; Conservative
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US-10-122-630-6
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y Sequence 178029, Application US/10027632

publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Delymorphisms in the Human Genome

FILE REFERENCE: 108927.129

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR PLICATION NUMBER: US 60/128,676

PRIOR PLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-24

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-29

PRIOR FILING DATE: 1999-09-29
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Publication No. US20303032611A1

GENERAL INFORMATION:
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Barbara A.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonaclectides
FILE REFERENCE: 0054.1088-019
CURRENT APPLICATION NUMBER: US/10/12,633
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: DCT/US01/10162
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR PILING DATE: 2001-03-31
PRIOR FILING DATE: 2001-03-31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 100.0%; Score 5; DB 15; Length 5; Similarity 100.0%; Pred. No. 9.4e+08; Conservative 0; Mismatches 0; Indels
0; Indels
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Gaps

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Indels

us-09-540-843-6.szlm200.rnpb

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APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Barbara A.
APPLICANT: Gilchrest, Mark S.
APPLICANT: Bler, Mark S.
APPLICANT: Bar, Mina
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054-1088-018
CURRENT APPLICATION NUMBER: US/10/122,630
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: PCT/US96/08386
PRIOR PILING DATE: 1995-06-06
PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR APPLICATION NUMBER: PCT/US01/10162
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                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic DNA Fragment
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
        PRIOR FILING DATE: 1996-06-03
PRIOR APPLICATION NUMBER: US 09/048,927
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2001-03-30
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                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 5; Conserv
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US-10-122-630-7/c
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US-10-122-633-3/c
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                                                                                                                                                                                                                                                                                LENGTH:
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Sequence 178043, Application US/10027632

PUBLICANT: Wang, US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-09-12

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-8

PRIOR PRIOR PRILICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

PRIOR PRIOR FILING DATE: 1999-08-09

PRIOR PRIOR PRILICATION NUMBER: US 60/146,002
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APPLICANT: Glichrest, Barbara A.
APPLICANT: Glichrest, Mark S.
APPLICANT: Taar, Minch A.
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligonucleotides
FILE REFERENCE: 0054-1088-018
CURRENT APPLICATION NUMBER: US 08/467,012
PRIOR APPLICATION NUMBER: US 08/467,012
PRIOR APPLICATION NUMBER: PCT/US96/08386
                                                                                                                                                                        Length 7;
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                                                                                                                                                                  100.0%; Score 5; DB 13; 100.0%; Pred. No. 6.7e+08
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                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-10-027-632-178043
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                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Human
SEQ ID NO 178029
LENGTH: 7
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Gaps

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100.0%; Score 5; DB 100.0%; Pred. No. 6.7 iive 0; Mismatches
                                                    FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/165,218
PRIOR PLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 178029
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-10-027-632-178029
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US-10-122-633-7/c

Sequence 7, Application US/10122633

Publication No. US2033032611A1

GENERAL INFORMATION:
APPLICANT: Eller, Mark S.
APPLICANT: Eller, Mark S.
TITLE OF INVENTION: Oligomuclectides
TITLE OF INVENTION: Oligomuclectides
FILE REFERENCE: 0054:1088-019
CURRENT APPLICATION NUMBER: US/10/122,633
CURRENT PILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: US 09/540,843
PRIOR FILING DATE: 2001-03-31
PRIOR FILING DATE: 2001-03-31
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PSELSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

100.0%; Score 5; DB 15; Length 7;

Best Local Similarity 100.0%; Pred. No. 6.7e+08;

Matches 5; Conservative 0; Mismatches 0; Indels
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APPLICANT: Gilchrest, Barbara A.
APPLICANT: Eller, Mark S.
APPLICANT: Eller, Mark S.
APPLICANT: Yaar, Mine
TITLE OF INVENTION: Method to Inhibit Cell Growth Using
TITLE OF INVENTION: Oligomucleotides
FILE REPERENCE: 0054-1088-019
CURRENT APPLICATION NUMBER: US 09/540,843
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: PCT/US01/10162
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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100.0%; Score 5; DB 15; L
Best Local Similarity 100.0%; Pred. No. 6.7e+08;
Matches 5; Conservative 0; Mismatches 0;
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Output
OS-10-122-633-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic DNA Fragment
US-10-122-633-7
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; Sequence 178029, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT' Wang, David G.

TITLE OF INVENTION: Telentification and Mapping of Single Nucleotide

TITLE OF INVENTION: Telentification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPREBREE: 10802-04-30

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-108-09

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
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Yant, Stephen

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                                                                                                                                                                                                      APPLICANT: HACKETT ET AL.

TITLE OF INVENTION: DNA-BASED TRANSPOSON SYSTEM FOR THE
TITLE OF INVENTION: INTRODUCTION OF NUCLEIC ACID INTO DNA OF A CELL
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSES: MUSTING, RAASCH & GEBHARDT, P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
CITY: MINNEAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/142,593
FILING DATE: 10-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/040,664
FILING DATE: 11-MAR-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/053,868
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/065,303
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/065,303
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 11-NAR-1998
ATTONEY/AGENT INPORMATION:

ANAME: CANNEDSON VICTORIES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: SANDBERG, VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 110.00450101
TELECOMMUICATION INFORMATION:
TELEPHONE: 612-305-1226
TELEFAX: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                ; Sequence 11, Application US/09142593; Patent No. US2002001015975A1
GENERAL INFORMATION: APPLICANT: HACKETT ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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STRANDEDNESS: single
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Best Local Similarity
Matches 5; Conserv
CATAC 5
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                                                                                  RESULT 13
US-09-142-593-11
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Sequence 17, Application US/09927886 Patent No. US20020103152A1 GENERAL INFORMATION:

US-09-927-886-17

2 CATAC 6

APPLICANT: Kay, Mark A.

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APPLICANT: Steer, Clifford
APPLICANT: Steer, Clifford
APPLICANT: Linehan-Exieers, Cheryle
APPLICANT: Linehan-Exieers, Cheryle
APPLICANT: McIvor, R.
APPLICANT: McIvor, R.
APPLICANT: McIvor, R.
TITLE OF INVENTION: Composition for Delivery of Compounds to Cells
FILE REFERENCE: 110.01330101
CURRENT APPLICATION NUMBER: US/9/861,014
CURRENT FILING DATE: 2001-05-19
PRIOR FILING DATE: 2000-05-19
PRIOR PRILING DATE: 2000-05-19
PRIOR PLING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: B
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TITLE OF INVENTION: Methods of In Vivo Gene Transfer Using a TITLE OF INVENTION: Sleeping Beauty Transposon System; FILE REPRENCE: STRAT-1600IP; CURRENT APPLICATION NUMBER: US/09/927,886; CURRENT FILING DATE: 1090-10.

FRIOR FILING DATE: 1099-10-28; FRIOR FAPLICATION NUMBER: 60/162,279; FRIOR FILING DATE: 1999-11-7; NUMBER OF SEQ ID NOS: 19; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 5; DB 9; Lot 100.0%; Pred. No. 5.9e+08;
                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: transposon repeat sequence US-09-927-886-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Direct repeat sequence US-09-861-014-6
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Patent No. US20020115216A1
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                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100...
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US-09-861-014-6
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